

SEARCH REQUEST FORM

111215

Requestor's Name: _____ Serial Number: _____
Date: _____ Phone: _____ Art Unit: _____

Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

STAFF USE ONLY

Date completed: 12/31/83
Searcher: [Signature]
Terminal time: _____
Elapsed time: 15 min
CPU time: _____
Total time: _____
Number of Searches: _____
Number of Databases: _____

Search Site

____ STIC
____ ☒ CM-1
____ Pre-S

Type of Search

____ N.A. Sequence
____ ☒ A.A. Sequence
____ Structure
____ Bibliographic

Vendors

____ IG
____ STN
____ Dialog
____ APS
____ Geninfo
____ SDC
____ DARC/Questel
____ ☒ Other

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STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 111215

TO: Phillip Gambel
Location: 8b03 / 9e12
Wednesday, December 31, 2003
Art Unit: 1644
Phone: 308-3997
Serial Number: 09 / 917410

From: Jan Delaval
Location: Biotech-Chem Library
Remsen Building
E01 - A51
Phone: 571-272-2504
jan.delaval@uspto.gov

Search Notes

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011215

Delavai, Jan

From: Gambel, Phillip
Sent: Wednesday, December 31, 2003 10:29 AM
To: Delavai, Jan
Subject: 09 / 917,410 multiple organ failure amd

jan

please perform a sequence and a sequence interference search for

09/ 917,410 multiple organ failure amd

SEQ ID NO: 2

SEQ ID NO: 4

SEQ ID NO: 5

SEQ ID NO: 6

thanx

phillip gambel
art unit 1644
308-3997

1644 mailbox 9e12

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 31, 2003, 10:29:11 ; Search time 8.36569 Seconds

(Without alignments)
2506.043 Million cell updates/sec

Title: US-09-917-410-2

Sequence: 1 DIOMTOSPSLSASVGDRTV.....EVTGGLSSPVTKSFNRGEC 218

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR 76:*
2: PIR1:*
3: PIR2:*
4: PIR3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	952.5	83.8	215	2 JE0242	Ig kappa chain NIG
2	919.5	80.9	215	2 JE0244	Ig kappa chain NIG
3	897.5	78.9	215	2 JE0243	Ig kappa chain NIG
4	878.5	77.3	215	2 A23746	Ig kappa chain V-I
5	872	76.7	216	2 JE0241	Ig kappa chain Am3
6	757	66.6	240	2 S06084	Ig kappa chain pre
7	740	65.1	218	2 S68241	Ig kappa chain V r
8	738	64.9	218	2 JCS810	Ig kappa chain V r
9	725	63.8	234	2 S14237	Ig kappa chain pre
10	724	63.7	230	2 S33161	Ig kappa chain -s
11	723	63.6	210	2 A56169	Ig kappa chain V r
12	722	63.5	220	2 A31790	Ig kappa chain V r
13	716.5	63.0	219	2 S38865	Ig kappa chain - m
14	713	62.7	234	2 S01320	Ig kappa chain pre
15	700.5	61.6	219	2 PC4203	Ig kappa chain (mo
16	697.5	61.3	219	2 SS2028	Ig kappa chain - m
17	697	61.3	214	2 S68212	Ig kappa chain (Ma
18	695.5	61.2	217	2 S42772	Ig kappa chain - m
19	692.5	60.9	225	2 S37484	Ig kappa chain - m
20	688.5	60.6	225	2 JI0029	Ig kappa chain pre
21	688.5	60.6	235	2 S25058	Ig kappa chain - m
22	687.5	60.5	219	2 S16112	Ig kappa chain V r
23	620.5	54.6	135	2 SS2059	Ig kappa chain - m
24	599	52.7	178	2 PT0219	Ig kappa chain V-C
25	568.5	50.0	229	2 A20969	Ig kappa chain pre
26	548	48.2	106	1 K3HU	Ig kappa chain C r
27	539.5	47.4	238	2 A49633	Ig kappa chain (W
28	537.5	47.3	197	2 S29593	Ig kappa chain C r
29	513	45.1	99	2 A37927	Ig kappa chain C r

30	512	45.0	127	2 S40367	Ig kappa chain V-U
31	507	44.6	99	2 S26653	Ig kappa chain C r
32	499	43.9	141	2 A49134	Ig kappa chain V-I
33	491	43.2	123	2 S40331	Ig kappa chain - h
34	490	43.1	108	2 B49047	Ig kappa chain V r
35	490	43.1	233	2 S29577	Ig kappa chain - r
36	489	43.0	109	2 S31998	Ig kappa chain - h
37	486	42.7	111	1 KVM508	Ig kappa chain V r
38	485	42.7	108	2 S44122	Ig kappa chain V r
39	485	42.7	139	2 S40365	Ig kappa chain - h
40	483	42.5	111	1 KVM569	Ig kappa chain V r
41	482	42.4	144	2 P10106	Ig kappa chain pre
42	480	42.2	111	1 KVM543	Ig kappa chain V r
43	480	42.2	125	2 S40333	Ig kappa chain V r
44	478	42.0	130	2 S40368	Ig kappa chain - h
45	474	41.7	111	1 KVM583	Ig kappa chain V r

ALIGNMENTS

RESULT 1

JE0242

Ig kappa chain NIG26 precursor - human

C/Species: Homo sapiens (man)

C/Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #ext_change 21-Jan-2000

C/Accession: JE0242

R/Alim: M.A.; Yamaki, S.; Hosain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda,

submitted to JIPID, November 1998

A/Description: Structure relationship of kappa type light chains with AL amyloidosis: Mu

A/Reference number: JE0241

A/Accession: JE0242

A/Molecule type: protein

A/Residues: 1-215 <ALI>

C/Superfamily: immunoglobulin V region; immunoglobulin homology

F;16-91/Domain: immunoglobulin homology <IMM>

Query Match 83.8%; Score 952.5; DB 2; Length 215;

Best Local Similarity 83.5%; Pred. No. 7.4e-55;

Matches 182; Conservative 15; Mismatches 18; Indels 3; Gaps 1;

QY	1	DIOMTOSPSLSASVGDRTVITTKASQSVYDGDSTMMNYOQKPGAPKILLIYAASNTLS 60	
DB	1	EIVLTQSPGTLISPERATLSCRASQSV---SNNYLAWYQKPGAPSLIILDAASSRAT 57	
QY	61	GIPSRFGSGSGDFTLTSSLOPEPFATYCCQSQSDEDPWTFGQTKVEIKRTVAAPSVF 120	
DB	58	GIIDRFSGSGSGITDFTLTSSGLEPDPFAYYCCQYRPPWTFGQTKVEIKRTVAAPSVF 117	
QY	121	IFPPSDQLKSGTASVAVCLINNFYPREAKVQWVDNALQSGNSQESVTEQDSKDSTYSLS 180	
DB	118	IFPPSDQLKSGTASVAVCLINNFYPREAKVQWVDNALQSGNSQESVTEQDSKDSTYSLS 177	
QY	181	STLTLSKADYEKHKVYACEVTHQGLSSPYTKSFNRGEC 218	
DB	178	STLTLSKADYEKHKVYACEVTHQGLSSPYTKSFNRGEC 215	

RESULT 2

JE0244

Ig kappa chain NIG2 precursor - human

C/Species: Homo sapiens (man)

C/Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #ext_change 21-Jan-2000

C/Accession: JE0244

R/Alim: M.A.; Hara, Y.; Hosain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.;

submitted to JIPID, November 1998

A/Description: A new subgroup of k type light chains (VKV) identified in cases of AL am

A/Reference number: JE0243

A/Accession: JE0244

A/Molecule type: protein

A/Residues: 1-215 <ALI>

C/Superfamily: immunoglobulin V region; immunoglobulin homology

F;16-90/Domain: immunoglobulin homology <IMM>

	Query March	80.9%;	Score 919.5;	DB 2;	Length 215;	
	Best Local Similarity	82.6%;	Pred. No. 1e-52;			
	Matches 181;	Conservative 14;	Mismatches 19;	Indels 5;	Gaps 2;	
QY	1	DIDMTGSSBSLSASVGDRAVTITTCAGSQSVDDGSINMMYYQQKGGKAPKLIIYAASNLES	60			
	:	:::::	:	:	:	:
Db	1	EVLVLTGPATISVSPGERATLSCRASQSV---HSNLAWYQKKGAARLLIYASTRAT	56			
QY	61	GIPRFSGSGSGGTDFTLTISLOPEDFATYYCCQDSNE-DPWTFCQGTFVEIKRTVAAPSV	119			
	:	: ::	:	:	:	:
Db	57	GIPARFGSGSGGTDFILTISSLOSIEDPALYYCQQTNTPTPLTFPGGTVEIKRTVAAPSV	116			
QY	120	FIFPPSDDELKSGTASVVCLINNFYPREAKYQMKNALQSNGSOGESYTEEDSCKDSTYSYL	179			
	:	: ::	:	:	:	:
Db	117	FIFPPSDDELKSGTASVVCLINNFYPREAKYQMKNALQSNGSOGESYTEEDSKDSTYSYL	176			
QY	180	SSTLTLSKADYEKKHYACETVHQGLSPVKSFNRGC	218			
	:	: ::	:	:	:	:
Db	177	SSTLTLSKADYEKKHYACEVTHQGLSPVKSFNRGC	215			

```

RESULT 3
JB0243
ig kappa chain NIG93 precursor - human
C:Species: Homo sapiens (man)
C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C:Accession: JB0243
R:Alt1, M.A.; Hara, Y.; Hossein, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazii, H.;
submitted to JRPID, November 1998
A:Description: A new subgroup of k type light chains (YKV) identified in cases of AL amyloidosis
A:Reference number: JB0243
A:Accession: JB0243
A:Molecule type: protein
A:Residues: 1-215 <Alt>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
#:16-90/Domain: immunoglobulin homology <IMM>

```

	Query Match	78.9%	Score 897.5	DB 2	Length 215
	Best Local Similarity	81.3%	Pred. No. 2.6e-51		
	Matches 178	Conservative 16	Mismatches 20	Indels 5	Gaps 2
QY	1	DIOMQSPSSLSASVGDRTVITCKASQSVYDGDSDYMNWYQKPGKAPKLLIYAASNIES	60		
DB	1	EIVMTQSPATLSVSGGERATLSCRASQSV---ATNVVWYMKLQAPRLILLYDASTRAT	56		
QY	61	GIPRSFSGSGCTDITLTISLQPDPAFYVCOGSDNEPDWFGSGTKVEIK-RTAAAPSV	119		
DB	57	GVPAPFSGSGSTETETLTISLQSEDFALYYCOHNNAMPPTGGGKTKETKRTVAAPSV	116		
QY	120	FIFPSPDEQLKSGTASVCLNNFYPYREAKVOMKYDNALQSGNSGSEVTEODSKDYSYL	179		
DB	117	FIFPSPDEQLKSGTASVCLNNFYPYREAKVOMKYDNALQSGNSGSEVTEODSKDYSYL	176		
QY	180	SSTLTLSKADYEKAKYACEVTHQGISPVYTSFNRGEC	218		
DB	177	SSTLTLSKADYEKAKYACEVTHQGISPVYTSFNRGEC	215		

```

RESULT 4
A23746
is kappa chain V-III (KAU cold agglutinin) - human
CSpecies: Homo sapiens (man)
CDate: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 21-Jan-2000
CAccession: A23746
RLeoni, J.; Ghiso, J.; Goni, F.; Frangione, B.
J. Biol. Chem. 266, 2836-2842, 1991
A>Title: The primary structure of the Fab fragment of protein KAU, a monoclonal
A.Reference number: A23746; MUID:91131575; PMID:1993660
A.Accession: A23746
A>Status: preliminary
A.Molecule type: protein
A.Residues: 1-215 <LEO>

```

C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-91/Domain: immunoglobulin homology <IMM>

	Query Match	77.3% Best Local Similarity 81.1%	Score 878.5	DB 2	Length 215
	Matches 176	Conservative 14	Mismatches 24	Indels 3	Gaps 1
QY	1	DIQNTGSPSSLSASVGDRAVTITTCASQSVYDGDSTYNNWTQOKRGPAPKLLIYANSLDES	60		
DB	1	EIVLTQSPATLSLSPGERATLISGASQSV--SSNYLAWYQOKRGAQAPRLIYDASSRAT	57		
QY	61	GIPERFSGSGSGDFTLTISLSLOPEDPATYXCQSQNSNEDPMTFGCGTKEIKRTVAASVF	120		
DB	58	GIPRFSGSGSGDFTLTISLSLEPEDPAVYVYGGQYGSPLTFGGGTKEIKRTVAASVF	117		
QY	121	IFPPSDSQLSGTSVYVCLNNFYPREAKYQWKYDNALQSGNSQESVTEEDSKDSTYSLS	180		
DB	118	IFPPSDQLQSGTSVYVGLNNFPPRPAKQWKMDNALQSGNSQESVTEEDSKDSTYSLS	177		
QY	181	STLTLSKADYEKHKVYACEVTHQGLSPVTKSPFRGE	217		
DB	178	STLTLSKADYEKHKVYACEVTHQGLSPVTKSPFRGE	214		

```

RESULT 5
JE0241
Ig kappa chain Am37 precursor - human
C/Species: Homo sapiens (man)
C/Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C/Accession: JE0241
R:Ailm, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda,
submitted to JIPIID, November 1998
A/Description: Structure relationship of kappa2type light chains with AL amyloidosis: Mu
A/Reference number: JE0241
A/Accession: JE0241
A/Molecule type: protein
A/Residues: 1-216 <Alt>
C/Superfamily: Immunoglobulin V region; immunoglobulin homology
F:16-92/Domain: Immunoglobulin homology <IIm>

```

Query Match	Similarity	76.7%	Score 672	DB 2	Length 216
Best Local	Similarity	78.4%	Pred. No. 1.2e-49		
Matches	171	Conservative	18	Mismatches	27
				Indels	2
				Gaps	2
QY	1	DIQMTQSESSLSASVGDNRVITTCASQSGVDYDGSYMMVYQKQFGAKPLLIYAASNLIES	60		
Db	1	DIVLQSPDFLAIVSGERATINCSSQGLVLSNKRKFLMWYQOKGQ--PKLLIW--ANVRES	58		
QY	61	GIPRSFGSSGCTPFTLLTSSLOPEDFATYYCOQSNEDPMFPGGQTKVEIKRTVAAPSVF	120		
Db	59	GVPDFRSGSGVDITLLTISMLQELVAVYICQOYISRTFYPGGQGRLEIKRTVAAPSVF	118		
QY	121	IFPSEDEQKSGTASVVCLLNFFYPREAKVQWKYNALQSGNSQSGSESVTEQDSKOSTYSLS	180		
Db	119	IFPPEDEQLKSGTASVVCLLNFFYPREAKVQWKYNALQSGNSQSGSESVTEQDSKOSTYSLS	178		
QY	181	STLTLSKADYERKKRYACEVTHQGLSSPVTSEFNRGEC	218		
Db	179	STLTLSKADYERKKRYACEVTHQGLSSPVTSEFNRGEC	216		

RESULT 6
S06084
Ig kappa chain precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 21-Jan-2000
C:Accession: S06084
R:Crowe, J.S.; Smith, M.A.; Cooper, H.J.
Nucleic Acids Res. 17, 7992, 1989
A:Title: Nucleotide sequence of Y3-Ag 1.2.3. rat myeloma immunoglobulin kappa chain cDNA
A:Reference number: S06084; MUID:190016888; PMID:2508667
A:Accession: S06084

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 31, 2003, 10:29:10 ; Search time 5.24906 Seconds

(without alignments)
1953.078 Million Cell updates/sec

Title: US-09-917-410-2

Perfect score: 1137

Sequence: 1 DIQMTGSPSSLSASVGDRT.....EVTHGGLSSPYTSFNRGEC 218

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	548	48.2	106	1 KAC_HUMAN	P01834 homo sapien
2	486	42.7	111	1 K3Q_MOUSE	P01667 mus musculu
3	483	42.5	111	1 K3Q_MOUSE	P01669 mus musculu
4	480	42.2	111	1 K3M_MOUSE	P01665 mus musculu
5	474	41.7	111	1 K3N_MOUSE	P01666 mus musculu
6	469	41.2	108	1 K1B_HUMAN	P01594 homo sapien
7	469	41.2	108	1 K1H_HUMAN	P01600 homo sapien
8	465.5	40.9	110	1 K3P_MOUSE	P01668 mus musculu
9	465	40.9	111	1 K3L_MOUSE	P01664 mus musculu
10	456	40.1	108	1 K1E_HUMAN	P01597 homo sapien
11	456	40.1	108	1 K1M_HUMAN	P01605 homo sapien
12	456	40.1	129	1 K1W_HUMAN	P04431 homo sapien
13	453	39.8	108	1 K1G_HUMAN	P01599 homo sapien
14	453	39.8	108	1 K1N_HUMAN	P01606 homo sapien
15	452	39.8	108	1 K1R_HUMAN	P01610 homo sapien
16	450	39.6	108	1 K1V_HUMAN	P04430 homo sapien
17	449	39.5	108	1 K1F_HUMAN	P01598 homo sapien
18	449	39.5	108	1 K1X_HUMAN	P01603 homo sapien
19	448	39.4	108	1 K1O_HUMAN	P01604 homo sapien
20	443	39.0	108	1 K1P_HUMAN	P01608 homo sapien
21	442	38.9	108	1 K1A_HUMAN	P01593 homo sapien
22	439	38.6	108	1 K1Y_HUMAN	P080362 homo sapien
23	438	38.5	108	1 K1S_HUMAN	P01611 homo sapien
24	435	38.3	108	1 K1L_HUMAN	P01660 homo sapien
25	433	38.1	111	1 K3H_MOUSE	P01596 homo sapien
26	432.5	38.0	107	1 K1T_HUMAN	P01612 homo sapien
27	431.5	38.0	109	1 K1I_HUMAN	P01661 mus musculu
28	431	37.9	131	1 K3I_MOUSE	P01609 homo sapien
29	429	37.7	108	1 K1Q_HUMAN	P01595 homo sapien
30	424	37.3	108	1 K1C_HUMAN	P01662 mus musculu
31	422	37.1	111	1 K3J_MOUSE	P06314 homo sapien
32	422	37.1	134	1 K1C_HUMAN	P06314 homo sapien
33	420	36.9	112	1 K3G_MOUSE	P01659 mus musculu

34	420	36.9	129	1 K1X_HUMAN	P04432 homo sapien
35	420	36.9	112	1 K3F_MOUSE	P01658 mus musculu
36	417	36.7	111	1 K3K_MOUSE	P01663 mus musculu
37	416	36.6	112	1 K1U_HUMAN	P01613 homo sapien
38	409.5	36.0	129	1 K3M_HUMAN	P01665 homo sapien
39	408	35.9	114	1 K4A_HUMAN	P01625 homo sapien
40	408	35.9	117	1 K1O_HUMAN	P01602 homo sapien
41	405	35.6	111	1 K3C_MOUSE	P01656 mus musculu
42	405	35.6	111	1 K3R_MOUSE	P01670 mus musculu
43	405	35.6	111	1 K3S_MOUSE	P01671 mus musculu
44	402	35.4	111	1 K3A_MOUSE	P01654 mus musculu
45	402	35.4	117	1 K1I_HUMAN	P01601 homo sapien

ALIGNMENTS

RESULT 1
KAC_HUMAN STANDARD; PRT; 106 AA.
ID KAC_HUMAN
AC P01834;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE 19 kappa chain C region.
GN IGKC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE (MYELOMA PROTEIN EU).
RX MEDLINE=71064023; PubMed=5489770;
RA Gottleib P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. VI. Amino
RT acid sequence of the light chain.";
RL Biochemistry 9:3155-3161(1970).
RN [2]
RP DISULFIDE BONDS.
RX MEDLINE=71064027; PubMed=4923144;
RA Gall W.E., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. X.
RT Intrachain disulfide bonds.";
RL Biochemistry 9:3188-3196(1970).
RN [3]
RP SEQUENCE (BENCE-JONES PROTEIN TI).
RX MEDLINE=72188439; PubMed=5027703;
RA Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
RT immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein
RT T1). IV. The complete amino acid sequence and its significance for
RT the mechanism of antibody production.";
RL Hoppe-Seyler's Z. Physiol. Chem. 353:189-208(1972).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=81042304; PubMed=675818;
RA Hietter P.A., Max E.E., Seidman J.G., Maizel J.V. Jr., Leder P.;
RT "Cloned human and mouse kappa immunoglobulin constant and J region
RT genes conserve homology in functional segments.";
RL Cell 22:197-207(1980).
RN [5]
RP SEQUENCE (BENCE-JONES PROTEIN ROY).
RA Hilschmann N., Barnikol H.U., Hees M., Langer B., Ponstingl H.,
RA Steinmetz-Kayne M., Suter L., Watanabe S.;
RT (In) Franek F., Shugar D. (eds.);
RL Gamma globulins: structure and function, pp.57-74, Academic Press,
RL New York (1969).
RN [6]
RP SEQUENCE (BENCE-JONES PROTEIN CUM).
RX MEDLINE=68242259; PubMed=5586923;
RA Hilschmann N.;
RT "The complete amino acid sequence of Bence Jones protein Cum (kappa-
RT type).";

RL Hoppe-Seyler's Z. Physiol. Chem. 348:1718-1722(1967).
 RN [7]
 RP SEQUENCE (BENCE-JONES PROTEIN AG).
 RX MEDLINE=69234734; PubMed=4893682;
 RA Titani K., Shinoda T., Putnam F.W.;
 RT "The amino acid sequence of a kappa type Bence-Jones protein. 3. The
 RL complete sequence and the location of the disulfide bridges.";
 RL J. Biol. Chem. 244:3550-3560(1969).
 RN [8]
 RP SEQUENCE (WALDENSTROM'S MACROGLOBULIN OU).
 RX MEDLINE=70201507; PubMed=5447531;
 RA Kohler H., Shimizu A., Paul C., Putnam F.W.;
 RT "Macroglobulin structure: variable sequence of light and heavy
 RL chains.";
 RL Science 169:56-59(1970).
 RN [9]
 RP SEQUENCE OF 1-33; 38-41 AND 62-80.
 RC TISSUE=Abdominal adipose tissue;
 RX PubMed=9588180;
 RA Olsen K.E., Sletten K., Westermarck P.;
 RT "Extended analysis of AL-amyloid protein from abdominal wall
 RL subcutaneous fat biopsy: kappa IV immunoglobulin light chain.";
 RL Biochem. Biophys. Res. Commun. 245:733-736(1998).
 CC -1- MISCELLANEOUS: THE EU SEQUENCE HAS THE INV (3) ALLOTYPIC MARKER,
 CC 45-ALA & 83-VAL. THE ROY SEQUENCE HAS THE INV (1,2) ALLOTYPIC
 CC MARKER, 45-ALA AND 83-LEU.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
 CC or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL: J00241; AAA58989.1; -
 DR EMBL: V00557; CAA23823.1; -
 DR PIR: B90562; K3HU.
 DR PDB: 1D5B; 09-FEB-00.
 DR PDB: 1D5I; 09-FEB-00.
 DR PDB: 1D6V; 04-OCT-00.
 DR PDB: 1HE2; 10-AUG-01.
 DR PDB: 1HE2; 12-MAR-97.
 DR PDB: 1I7Z; 08-AUG-01.
 DR PDB: 1M1M; 15-MAY-97.
 DR Genew; HGNC:5716; IGKC.
 DR MIM; 147200; -
 DR GO; GO:0003823; P:antigen binding activity; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003597; IG cl.
 DR InterPro; IPR003006; IG_MHC.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00407; Igcl; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Immunoglobulin domain; Immunoglobulin C region; 3D-structure.
 FT NON TER 1 1
 FT DOMAIN 5 102 IG-LIKE.
 FT DISULFID 26 86
 FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
 FT VARIANT 83 83 V -> L (IN INV(1,2) MARKER).
 FT /FTID=VAR_003897.
 FT CONFLICT 14 14 D -> N (IN REF. 7 AND 8).
 FT CONFLICT 57 57 E -> Q (IN REF. 5 AND 6).
 SQ SEQUENCE 106 AA; 11609 MW; 51984D1FD372CE8 CRC64;
 Query Match 48.2%; Score 548; DB 1; Length 106;
 Best Local Similarity 100.0%; Pred. No. 2.8e-38;
 Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 TAAAPSVFIPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 60
 QY 173 KDSYLSSTLTLSKADYEKKHYVACEYTHQGLSSPYTKSFNRGEC 218
 Db 61 KDSYLSSTLTLSKADYEKKHYVACEYTHQGLSSPYTKSFNRGEC 106
 RESULT 2
 KV30_MOUSE STANDARD; PRT; 111 AA.
 ID KV30_MOUSE
 AC P01667;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-II region PC 6308.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxId=10090;
 RX MEDLINE=79073152; PubMed=103003;
 RA Weigert M., Gattaman L., Loh E., Schilling J., Hood L.E.;
 RT "Rearrangement of genetic information may produce immunoglobulin
 RL diversity.";
 RL Nature 276:785-790(1978).
 DR PIR: C01937; KMS08.
 DR HSSP; P80362; 1WTL.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 39 53 FRAMEWORK-2.
 FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 61 92 FRAMEWORK-3.
 FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING-3.
 FT DISULFID 102 111 FRAMEWORK-4.
 FT NON TER 111 111 BY SIMILARITY.
 SQ SEQUENCE 111 AA; 12071 MW; 7A4ADE4D6C256D29 CRC64;
 Query Match 42.7%; Score 486; DB 1; Length 111;
 Best Local Similarity 80.2%; Pred. No. 3.4e-33;
 Matches 89; Conservative 10; Mismatches 12; Indels 0; Gaps 0;
 QY 1 DIOMTQSPSSLSASVGDVITTCASQSGVDPSYMMWYQKQKAPKLIYASNLDS 60
 Db 1 DIVLTQSPASLAIVSGQATISCRASQSGVDPSYMMWYQKQKAPKLIYASNLDS 60
 QY 61 GIPSRFSGSGGTDTFTLTSSLOPEDFATYYCQGSNEDPMTFGGTQYKIK 111
 Db 61 GIPARFSGSGGTDTFTLTINHPVEEDATYYCQGSNEDPMTFGGTQYKIK 111
 RESULT 3
 KV30_MOUSE STANDARD; PRT; 111 AA.
 ID KV30_MOUSE
 AC P01669;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-II region PC 7769.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxId=10090;
 RX [1]

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 31, 2003, 10:29:10 ; Search time 18.5357 Seconds

(without alignments)
3034.973 Million cell updates/sec

Title: US-09-917-410-2

Sequence: 1 DIOMTQSPSSLSASVGDRTV.....ETHHGLSSPVTSSFRNGEC 218

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SP archaea:*
2: SP bacteria:*
3: SP fungi:*
4: SP human:*
5: SP invertebrate:*
6: SP mammal:*
7: SP mbc:*
8: SP organelle:*
9: SP phage:*
10: SP plant:*
11: SP rodent:*
12: SP virus:*
13: SP vertebrate:*
14: SP unclassified:*
15: SP virus:*
16: SP bacteriophage:*
17: SP archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES:

Result No.	Score	Query Match	Length	DB ID	Description
1	929	81.7	234	4	Q8NEK1
2	899.5	79.1	239	4	Q8TCD0
3	898.5	79.0	239	4	Q8NEK0
4	747	65.7	233	11	Q91WS9
5	744	65.4	234	11	Q8R062
6	737	64.8	234	11	Q91WF8
7	733	64.5	214	11	Q91R15
8	726	63.9	234	11	Q8VCP0
9	707.5	62.2	238	11	Q99M37
10	701.5	61.7	238	11	Q8VC16
11	701.5	61.7	239	11	Q8VC55
12	685.5	60.3	235	11	Q91W12
13	683.5	60.1	239	11	Q8K0F8
14	664	58.4	234	11	Q8R028
15	494	43.4	108	4	Q9U177
16	472.5	41.6	107	4	Q96SA9

17	451.5	39.7	233	4	Q8TBC9	Q8TBC9 homo sapien
18	451	39.7	108	4	Q9U170	Q9U170 homo sapien
19	447.5	39.4	107	4	Q9U181	Q9U181 homo sapien
20	446	39.2	116	4	Q96EP6	Q96EP6 homo sapien
21	445.5	39.2	237	4	Q8WTR6	Q8WTR6 homo sapien
22	443	39.0	236	4	Q8NEJ1	Q8NEJ1 homo sapien
23	442.5	38.9	237	4	Q8WUK4	Q8WUK4 homo sapien
24	431	37.9	108	4	Q9U179	Q9U179 homo sapien
25	425.5	37.4	233	4	Q8N5F4	Q8N5F4 homo sapien
26	425	37.4	234	4	Q8N355	Q8N355 homo sapien
27	410	36.1	111	11	Q92OE9	Q92OE9 mus musculus
28	408.5	35.9	236	4	Q96E61	Q96E61 mus musculus
29	404	35.5	240	4	Q8WUK3	Q8WUK3 mus musculus
30	396.5	34.9	235	11	Q99M11	Q99M11 mus musculus
31	388	34.1	109	11	Q92OE6	Q92OE6 mus musculus
32	387.5	34.1	109	4	Q9U178	Q9U178 mus musculus
33	385.5	33.9	112	11	Q8K1F2	Q8K1F2 mus musculus
34	383.5	33.7	112	11	Q8K1F3	Q8K1F3 mus musculus
35	382.5	33.6	114	11	Q8K1F1	Q8K1F1 mus musculus
36	382	33.6	108	4	Q9U183	Q9U183 mus musculus
37	380	33.4	238	11	Q9QYF0	Q9QYF0 mus musculus
38	379	33.3	103	11	Q9U180	Q9U180 mus musculus
39	378.5	33.3	134	11	Q8VDD0	Q8VDD0 mus musculus
40	370	32.5	107	11	Q9U184	Q9U184 mus musculus
41	369.5	32.5	109	4	Q9U185	Q9U185 mus musculus
42	368.5	32.4	109	4	Q9U186	Q9U186 mus musculus
43	368	32.4	108	11	Q8V1J0	Q8V1J0 mus musculus
44	363.5	32.0	233	4	Q96169	Q96169 mus sapien
45	360	31.7	114	4	Q9U180	Q9U180 homo sapien

ALIGNMENTS

RESULT 1

Q8NEK1 PRELIMINARY; PRT; 234 AA.

AC Q8NEK1;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC030813; AAH30813.1; -
DR InterPro; IPR007110; IG_1ike.
DR InterPro; IPR003597; IG_C1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG_2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGY; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25530 MW; 631E8DE8FD132F8 CRC64;

Query Match 81.7%; Score 929; DB 4; Length 234;
Best Local Similarity 82.1%; Pred. No. 1e-73;

Matches 179; Conservative 19; Mismatches 16; Indels 4; Gaps 1;

Qy 1 DIOMTQSPSSLSASVGDRTVITCKASQSYDSDSYNNYQKRGKAPKLLIYAASNLIES 60
Db 21 EIMTQSPATLSVSPERATLSCRASQSV---TSNLAWQGFPGSPRIVITGASRRAS 76
Qy 61 GIPSRFGSGSGTDFLTITISLOPEDFATYYCCQSNEDPWTFGQGTKEIKRTVAAPSV 120

```

Db      77  GVPARFSGSGSGTFFLTITSLQSDFAVYVYCOQNKMPHFQGTGKIDIKRTVAAPSVF
Qy      121  IFPPDEDLKSGTASVVCILNNFYREAKVQKVNALQSGNSQSDSEDSKSTYSL 180
Db      137  IFPPDEDLKSGTASVVCILNNFYREAKVQKVNALQSGNSQSDSEDSKSTYSL 196
Qy      181  STLTLSKADYEKHKYVACEVTHQGLSSPVTGSFNRGEC 218
Db      197  STLTLSKADYEKHKYVACEVTHQGLSSPVTGSFNRGEC 234

```

RESULT 2

```

O8TCDD0 PRELIMINARY; PRT; 239 AA.
AC O8TCDD0;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strauberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC022362; AAH22362.1; -.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig_2.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
DR Hypothetical protein.
SQ SEQUENCE 239 AA; 26234 MW; FACEDCA3B0871D CRC64;

```

Query Match 79.1%; Score 899.5; DB 4; Length 239;

Best Local Similarity 77.2%; Pred. No. 4,1e-71;

Matches 169; Conservative 24; Mismatches 25; Indels 1; Gaps 1;

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Qy      1  DIQMTQSPSSLSASVGDRVTITCKAQSQSDY-DGDSYMNWYQOKPKLIIYAASNLE 59
Db      21  DVMTQSPSLPLVTIGQPASISCRSTQSLVSDGNTYLNWFQQRFGSGPRRLIYKVSNRD 80
Qy      60  SGIPSRFSGSGSGTDFLTITSLQPEDPATYVYCOQSNEDPMTFGQGTKEIKRTVAAPSV 119
Db      81  SGVPRFRFSGSGSGTDFLTITSLQPEDPATYVYCOQSNEDPMTFGQGTKEIKRTVAAPSV 140
Qy      120  FIFPPSDEQLKSGTASVVCILNNFYPREAKVQKVNALQSGNSQSDSEDSKSTYSL 179
Db      141  FIFPPSDEQLKSGTASVVCILNNFYPREAKVQKVNALQSGNSQSDSEDSKSTYSL 200
Qy      180  SSSLTSLKADYEKHKYVACEVTHQGLSSPVTGSFNRGEC 218
Db      201  SSSLTSLKADYEKHKYVACEVTHQGLSSPVTGSFNRGEC 239

```

RESULT 3

```

O8NEKO PRELIMINARY; PRT; 239 AA.
AC O8NEKO;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;

```

```

RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RA Strauberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC030814; AAH30814.1; -.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig_2.
DR SMART; SM00407; Igv; 1.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
DR Hypothetical protein.
SQ SEQUENCE 239 AA; 26024 MW; F5E20AD3B0552C0A CRC64;

```

Query Match 79.0%; Score 898.5; DB 4; Length 239;

Best Local Similarity 79.0%; Pred. No. 5e-71;

Matches 173; Conservative 18; Mismatches 27; Indels 1; Gaps 1;

```

Qy      1  DIQMTQSPSSLSASVGDRVTITCKAQSQSDY-DGDSYMNWYQOKPKLIIYAASNLE 59
Db      21  DVMTQSPSLPLVTIGQPASISCRSTQSLVSDGNTYLNWFQQRFGSGPOLLILYGSNRA 80
Qy      60  SGIPSRFSGSGSGTDFLTITSLQPEDPATYVYCOQSNEDPMTFGQGTKEIKRTVAAPSV 119
Db      81  SGVPRFRFSGSGSGTDFLTITSLQPEDPATYVYCOQSNEDPMTFGQGTKEIKRTVAAPSV 140
Qy      120  FIFPPSDEQLKSGTASVVCILNNFYPREAKVQKVNALQSGNSQSDSEDSKSTYSL 179
Db      141  FIFPPSDEQLKSGTASVVCILNNFYPREAKVQKVNALQSGNSQSDSEDSKSTYSL 200
Qy      180  SSSLTSLKADYEKHKYVACEVTHQGLSSPVTGSFNRGEC 218
Db      201  SSSLTSLKADYEKHKYVACEVTHQGLSSPVTGSFNRGEC 239

```

RESULT 4

```

O91WS9 PRELIMINARY; PRT; 233 AA.
AC O91WS9;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Hypothetical 25.8 kDa protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strauberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013496; AAH13496.1; -.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig_2.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
DR Hypothetical protein.
FT NON_TER
SQ SEQUENCE 233 AA; 25781 MW; B1C184DA149A16EB CRC64;

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Query Match 65.7%; Score 747; DB 11; Length 233;

Best Local Similarity 64.7%; Pred. No. 9,8e-58;

Matches 141; Conservative 28; Mismatches 45; Indels 4; Gaps 1;

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Qy      1  DIQMTQSPSSLSASVGDRVTITCKAQSQSDY-DGDSYMNWYQOKPKLIIYAASNLE 60

```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 31, 2003, 10:33:16 / Search time 22.4725 Seconds

(Without alignments)
1539.764 Million cell updates/sec

Title: US-09-917-410-2

Sequence: 1 D1QMTQSPSSLSASVGRVT.....EYTHQGLSPVTSFNRGEC 218

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

1: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
4: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
5: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
6: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
7: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
8: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
9: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
10: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
11: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
12: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
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14: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
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20: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1137	100.0	218	18	AAW13563
2	1113	97.9	238	21	AAW90932
3	1113	97.9	238	23	ABR74901
4	1112	97.8	238	21	AAW90930
5	1112	97.8	238	23	ABR74899
6	1108	97.4	218	20	AAW95658
7	1108	97.4	218	21	AAW85200
8	1108	97.4	218	22	ABR76947
9	1108	97.4	238	21	AAW90931

10	1108	97.4	238	23	ABR74900	Humanised anti-Fas
11	1101	96.8	218	14	AAK33312	Humanised Mac11 Ve
12	1085	95.4	218	20	AAW50030	Human E27 anti-IGF
13	1085	95.4	218	20	AAW95660	Mus musculus anti-
14	1085	95.4	218	20	AAW95662	Mus musculus anti-
15	1085	95.4	218	21	ABR07472	Amino acid sequenc
16	1085	95.4	218	22	ABR74211	E27 anti-IGF antib
17	1082	95.2	218	20	AAW95669	Mus musculus anti-
18	1082	95.2	218	20	AAW95664	Mus musculus anti-
19	1082	95.2	218	22	ABR47087	Anti-IGF antibody
20	1082	95.2	218	22	ABR76949	Full length light
21	1082	95.2	218	22	ABR76951	Full length light
22	1082	95.2	218	22	ABR76953	Variable light cha
23	1082	95.2	218	22	ABR76958	Variable light cha
24	1050	92.3	238	19	AAW83034	Humanised anti-Fas
25	1050	92.3	238	21	AAW83032	Humanised anti-Fas
26	1050	92.3	238	21	AAW90927	Humanised anti-Fas
27	1050	92.3	238	23	ABR74896	Humanised anti-Fas
28	1050	92.3	238	23	ABR74892	Humanised anti-Fas
29	1045	91.9	238	19	AAW83031	Humanised anti-Fas
30	1045	91.9	238	21	AAW83032	Humanised anti-Fas
31	1045	91.9	238	21	AAW90922	Humanised anti-Fas
32	1045	91.9	238	23	ABR74891	Humanised anti-Fas
33	1045	91.9	238	23	ABR74897	Humanised anti-Fas
34	1032	90.8	214	21	AAW93735	Humanised anti-Fas
35	1032	90.8	238	19	AAW83032	The kappa chain of
36	1032	90.8	238	21	AAW83032	Humanised anti-Fas
37	1032	90.8	238	21	AAW90923	Humanised anti-Fas
38	1032	90.8	238	23	ABR74892	Humanised anti-Fas
39	1032	90.8	238	23	ABR74898	Humanised anti-Fas
40	1031	90.7	238	19	AAW83035	Humanised anti-Fas
41	1031	90.7	238	21	AAW83035	Humanised anti-Fas
42	1031	90.7	238	21	AAW90928	Humanised anti-Fas
43	1031	90.7	238	23	ABR74897	Humanised anti-Fas
44	1031	90.7	238	23	ABR74893	Humanised anti-Fas
45	1030	90.6	238	19	AAW83033	Anti-Fas humanised

ALIGNMENTS

RESULT 1	AAW13563 standard; Protein; 218 AA.
ID	AAW13563
AC	AAW1563;
XX	
DT	03-JUN-1997 (first entry)
XX	
DE	Humanised anti-L-selectin antibody HuDreg 55 light chain.
XX	
KM	L-selectin; humanised antibody; HuDreg 55; acute organ damage;
KW	organ failure; poly-trauma; haemorrhagic-traumatic shock.
XX	
OS	Chimeric Mus sp.;
OS	Chimeric Homo sapiens.
XX	
PN	WO9706822-A1.
XX	
PD	27-FEB-1997.
XX	
PF	14-AUG-1996; 96WO-US13152.
XX	
PR	27-DEC-1995; 95US-0578953.
PR	17-AUG-1995; 95EP-0112895.
PR	19-SEP-1995; 95EP-0114696.
XX	
PA	(BOEP) BOEHRINGER MANNHEIM GMBH.
PA	(PROT-) PROTEIN DESIGN LABS INC.
XX	
PI	Co M, Haselbeck A, Martin U, Schumacher G;
XX	
DR	WPI; 1997-165036/15.

DR N-PSDB; AAT61280.

XX using anti-selectin antibody to prevent acute organ damage and

PT multiple organ failure - during extracorporeal circulation or

PT following polytrauma, e. g. haemorrhagic-traumatic shock

XX

PS Disclosure; Page 32-33; 52pp; English.

XX

CC Humanised anti-I-selectin antibody Hudreg 55 comprises 2 light

CC chains each having the sequence given in AAM13563 and 2 heavy chains

CC each having the sequence given in AAM13564. These are encoded by the

CC cDNA clones given in AAT61280 and AAT61281. Hudreg 55 can be used to

CC prevent multiple organ failure associated with polytrauma and for

CC the prevention of acute organ damage associated with extracorporeal

CC blood circulation. The antibody inhibits interaction between the

CC carbohydrate-recognising domain of the selectin and the

CC corresponding cell surface receptor.

XX

Sequence 218 AA:

Query Match 100.0%; Score 1137; DB 18; Length 218;

Best Local Similarity 100.0%; Pred. No. 1e-57; Mismatches 0; Indels 0; Gaps 0;

Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCKASQSVYDGDSDYNNMWYQKPKAKPLIYAASNLES 60

DB 1 DIQMTQSPSSLSASVGRVTITCKASQSVYDGDSDYNNMWYQKPKAKPLIYAASNLES 60

QY 61 GIPSPFSSGSGGTDTLTITSSLOPEDPATYTCQSNEDPWFPGGQTKYEIKRTVAAPSVF 120

DB 61 GIPSPFSSGSGGTDTLTITSSLOPEDPATYTCQSNEDPWFPGGQTKYEIKRTVAAPSVF 120

QY 121 IFPPSDEQLKSGTASVCLNNFYPREAKVQMKVDNALQSGNSQESVTEQDSKSTYLS 180

DB 121 IFPPSDEQLKSGTASVCLNNFYPREAKVQMKVDNALQSGNSQESVTEQDSKSTYLS 180

QY 181 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNNGEC 218

DB 181 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNNGEC 218

RESULT 2

AAM90932

ID AAM90932 standard; Protein; 238 AA.

XX

AC AAM90932;

XX

DT 08-AUG-2000 (first entry)

XX

DE Humanised anti-Fas designed light chain Leu 3 protein.

XX

XX Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;

KW anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiac;

KW dermatological; immunosuppressive; thyromimetic; antineuritic; anti-Fas;

KW nephrotropic; antifertility; neuroprotective; antiarteriosclerotic;

KW hepatocarcinoma; humanized; apoptosis; systemic lupus erythematosus;

KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;

KW Sjogren's syndrome; anemia; Addison's disease; scleroderma; sterility;

KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;

KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;

KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;

KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.

XX

OS Synthetic.

XX

PN EP990663-A2.

XX

XX 05-APR-2000.

PD

XX

PF 29-SEP-1999; 99EP-0307711.

XX

XX 30-SEP-1998; 98JP-0276881.

PR

XX 30-SEP-1998; 98JP-0276882.

XX (SANYI) SANKYO CO LTD.

PA

XX Serizawa N, Hatayama H, Nakahara K, Tamaki I, Takahashi T;

PI

XX WPI; 2000-258930/23.

DR

XX N-PSDB; AAM1633.

XX

PT New humanized anti-Fas antibody, useful for treating or preventing e.g.

PT inflammatory or autoimmune disease, induces apoptosis selectively in

PT cells with abnormal Fas-Fas ligand systems

XX

PS Claim 3; Page 161-162; 263pp; English.

XX

CC This invention describes a novel humanized anti-Fas antibody-like

CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas

CC ligand system, by binding to Fas on the cell surface, and prevents

CC apoptosis in cells with a normal system, by inhibiting binding between

CC Fas and its ligand. The products of the invention have anti-inflammatory,

CC anti-anemic, antidiabetic, anti-allergic, anti-arthritic, antiviral,

CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,

CC antineuritic, nephrotropic, antifertility, neuroprotective,

CC antiarteriosclerotic, cardiac and hepatotropic activity. (I) induce

CC apoptosis by binding to cell surface Fas or inhibit it by competitive

CC inhibition of ligand binding. (I) are used to treat and/or prevent

CC diseases associated with the Fas/Fas ligand system, especially systemic

CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft

CC versus host disease, Sjogren's syndrome, pernicious or hypoplastic

CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's

CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,

CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin

CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,

CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral

CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively

CC inhibit apoptosis in normal cells but selectively induce it in abnormal

CC cells. They bind to both human and murine Fas, so can be evaluated in

CC murine disease models. (I) act on the active site of Fas, i.e. they mimic

CC the native ligand, do not induce liver disease, and have reduced risk of

CC inducing a human anti-murine antibody response. This sequence represents

CC a humanised anti-Fas antibody light chain construct designated Leu 3

CC which is described in the method of the invention.

XX

Sequence 238 AA:

Query Match 97.9%; Score 113; DB 21; Length 238;

Best Local Similarity 98.6%; Pred. No. 2.5e-56;

Matches 215; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCKASQSVYDGDSDYNNMWYQKPKAKPLIYAASNLES 60

DB 21 DIQMTQSPSSLSASVGRVTITCKASQSVYDGDSDYNNMWYQKPKAKPLIYAASNLES 80

QY 61 GIPSPFSSGSGGTDTLTITSSLOPEDPATYTCQSNEDPWFPGGQTKYEIKRTVAAPSVF 120

DB 81 GIPSPFSSGSGGTDTLTITSSLOPEDPATYTCQSNEDPWFPGGQTKYEIKRTVAAPSVF 140

QY 121 IFPPSDEQLKSGTASVCLNNFYPREAKVQMKVDNALQSGNSQESVTEQDSKSTYLS 180

DB 141 IFPPSDEQLKSGTASVCLNNFYPREAKVQMKVDNALQSGNSQESVTEQDSKSTYLS 200

QY 181 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNNGEC 218

DB 201 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNNGEC 238

RESULT 3

ABB74901

ID ABB74901 standard; Protein; 238 AA.

XX

XX ABB74901;

AC

XX

DT 26-APR-2002 (first entry)

XX

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 31, 2003, 10:32:16 ; Search time 16.8954 Seconds
(without alignments)
2588.856 Million cell updates/sec

Title: US-09-917-410-2

Perfect score: 1137
Sequence: 1 DQMTGSPSSLASVGDVLT.....EVTGGLSPVTKSFNRGEC 218

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 733937 seqs, 200641211 residues

Total number of hits satisfying chosen parameters: 733937

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications_AA:*

- 1: /cgn2_6/ptodata/1/pubppaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubppaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/1/pubppaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/1/pubppaa/US06_PUBCOMB.pep:*
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- 9: /cgn2_6/ptodata/1/pubppaa/US09_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/1/pubppaa/US09C_PUBCOMB.pep:*
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- 12: /cgn2_6/ptodata/1/pubppaa/US09_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1137	100.0	218	9	US-09-917-410-2
2	1113	97.9	238	12	US-10-384-933-131
3	1113	97.9	238	15	US-10-216-484-131
4	1112	97.8	238	12	US-10-384-933-127
5	1112	97.8	238	15	US-10-216-484-127
6	1108	97.4	218	9	US-09-802-077-9
7	1108	97.4	218	9	US-09-802-096-9
8	1108	97.4	218	9	US-09-920-171-13
9	1108	97.4	218	11	US-09-925-179-9
10	1108	97.4	218	12	US-10-113-996-13
11	1108	97.4	238	12	US-10-384-933-129
12	1108	97.4	238	15	US-10-216-484-129
13	1095	96.3	218	11	US-09-925-179-67
14	1085	95.4	218	12	US-10-292-869-1
15	1085	95.4	218	12	US-09-792-938-1

16	1082	95.2	218	9	US-09-920-171-15	Sequence 15, Appl
17 <td>1082<td>95.2<td>218<td>9<td>US-09-920-171-17</td><td>Sequence 17, Appl</td></td></td></td></td>	1082 <td>95.2<td>218<td>9<td>US-09-920-171-17</td><td>Sequence 17, Appl</td></td></td></td>	95.2 <td>218<td>9<td>US-09-920-171-17</td><td>Sequence 17, Appl</td></td></td>	218 <td>9<td>US-09-920-171-17</td><td>Sequence 17, Appl</td></td>	9 <td>US-09-920-171-17</td> <td>Sequence 17, Appl</td>	US-09-920-171-17	Sequence 17, Appl
18 <td>1082<td>95.2<td>218<td>9<td>US-09-920-171-19</td><td>Sequence 19, Appl</td></td></td></td></td>	1082 <td>95.2<td>218<td>9<td>US-09-920-171-19</td><td>Sequence 19, Appl</td></td></td></td>	95.2 <td>218<td>9<td>US-09-920-171-19</td><td>Sequence 19, Appl</td></td></td>	218 <td>9<td>US-09-920-171-19</td><td>Sequence 19, Appl</td></td>	9 <td>US-09-920-171-19</td> <td>Sequence 19, Appl</td>	US-09-920-171-19	Sequence 19, Appl
19 <td>1082<td>95.2<td>218<td>9<td>US-09-920-171-24</td><td>Sequence 24, Appl</td></td></td></td></td>	1082 <td>95.2<td>218<td>9<td>US-09-920-171-24</td><td>Sequence 24, Appl</td></td></td></td>	95.2 <td>218<td>9<td>US-09-920-171-24</td><td>Sequence 24, Appl</td></td></td>	218 <td>9<td>US-09-920-171-24</td><td>Sequence 24, Appl</td></td>	9 <td>US-09-920-171-24</td> <td>Sequence 24, Appl</td>	US-09-920-171-24	Sequence 24, Appl
20 <td>1082<td>95.2<td>218<td>12<td>US-10-113-996-15</td><td>Sequence 15, Appl</td></td></td></td></td>	1082 <td>95.2<td>218<td>12<td>US-10-113-996-15</td><td>Sequence 15, Appl</td></td></td></td>	95.2 <td>218<td>12<td>US-10-113-996-15</td><td>Sequence 15, Appl</td></td></td>	218 <td>12<td>US-10-113-996-15</td><td>Sequence 15, Appl</td></td>	12 <td>US-10-113-996-15</td> <td>Sequence 15, Appl</td>	US-10-113-996-15	Sequence 15, Appl
21 <td>1082<td>95.2<td>218<td>12<td>US-10-113-996-17</td><td>Sequence 17, Appl</td></td></td></td></td>	1082 <td>95.2<td>218<td>12<td>US-10-113-996-17</td><td>Sequence 17, Appl</td></td></td></td>	95.2 <td>218<td>12<td>US-10-113-996-17</td><td>Sequence 17, Appl</td></td></td>	218 <td>12<td>US-10-113-996-17</td><td>Sequence 17, Appl</td></td>	12 <td>US-10-113-996-17</td> <td>Sequence 17, Appl</td>	US-10-113-996-17	Sequence 17, Appl
22 <td>1082<td>95.2<td>218<td>12<td>US-10-113-996-19</td><td>Sequence 19, Appl</td></td></td></td></td>	1082 <td>95.2<td>218<td>12<td>US-10-113-996-19</td><td>Sequence 19, Appl</td></td></td></td>	95.2 <td>218<td>12<td>US-10-113-996-19</td><td>Sequence 19, Appl</td></td></td>	218 <td>12<td>US-10-113-996-19</td><td>Sequence 19, Appl</td></td>	12 <td>US-10-113-996-19</td> <td>Sequence 19, Appl</td>	US-10-113-996-19	Sequence 19, Appl
23 <td>1082<td>95.2<td>218<td>12<td>US-10-113-996-24</td><td>Sequence 24, Appl</td></td></td></td></td>	1082 <td>95.2<td>218<td>12<td>US-10-113-996-24</td><td>Sequence 24, Appl</td></td></td></td>	95.2 <td>218<td>12<td>US-10-113-996-24</td><td>Sequence 24, Appl</td></td></td>	218 <td>12<td>US-10-113-996-24</td><td>Sequence 24, Appl</td></td>	12 <td>US-10-113-996-24</td> <td>Sequence 24, Appl</td>	US-10-113-996-24	Sequence 24, Appl
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32 <td>1031<td>90.7</td><td>218</td><td>12<td>US-10-353-708-57</td><td>Sequence 57, Appl</td></td></td>	1031 <td>90.7</td> <td>218</td> <td>12<td>US-10-353-708-57</td><td>Sequence 57, Appl</td></td>	90.7	218	12 <td>US-10-353-708-57</td> <td>Sequence 57, Appl</td>	US-10-353-708-57	Sequence 57, Appl
33 <td>1031<td>90.7</td><td>218</td><td>15<td>US-10-171-452A-39</td><td>Sequence 39, Appl</td></td></td>	1031 <td>90.7</td> <td>218</td> <td>15<td>US-10-171-452A-39</td><td>Sequence 39, Appl</td></td>	90.7	218	15 <td>US-10-171-452A-39</td> <td>Sequence 39, Appl</td>	US-10-171-452A-39	Sequence 39, Appl
34 <td>1031<td>90.7</td><td>218</td><td>15<td>US-10-171-452A-57</td><td>Sequence 57, Appl</td></td></td>	1031 <td>90.7</td> <td>218</td> <td>15<td>US-10-171-452A-57</td><td>Sequence 57, Appl</td></td>	90.7	218	15 <td>US-10-171-452A-57</td> <td>Sequence 57, Appl</td>	US-10-171-452A-57	Sequence 57, Appl
35 <td>1031<td>90.7</td><td>238</td><td>12<td>US-10-384-933-109</td><td>Sequence 109, App</td></td></td>	1031 <td>90.7</td> <td>238</td> <td>12<td>US-10-384-933-109</td><td>Sequence 109, App</td></td>	90.7	238	12 <td>US-10-384-933-109</td> <td>Sequence 109, App</td>	US-10-384-933-109	Sequence 109, App
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38 <td>1031<td>90.7</td><td>238</td><td>15<td>US-10-216-484-109</td><td>Sequence 109, App</td></td></td>	1031 <td>90.7</td> <td>238</td> <td>15<td>US-10-216-484-109</td><td>Sequence 109, App</td></td>	90.7	238	15 <td>US-10-216-484-109</td> <td>Sequence 109, App</td>	US-10-216-484-109	Sequence 109, App
39 <td>1031<td>90.7</td><td>238</td><td>15<td>US-10-171-452A-38</td><td>Sequence 38, Appl</td></td></td>	1031 <td>90.7</td> <td>238</td> <td>15<td>US-10-171-452A-38</td><td>Sequence 38, Appl</td></td>	90.7	238	15 <td>US-10-171-452A-38</td> <td>Sequence 38, Appl</td>	US-10-171-452A-38	Sequence 38, Appl
40 <td>1031<td>90.7</td><td>238</td><td>15<td>US-10-171-452A-56</td><td>Sequence 56, Appl</td></td></td>	1031 <td>90.7</td> <td>238</td> <td>15<td>US-10-171-452A-56</td><td>Sequence 56, Appl</td></td>	90.7	238	15 <td>US-10-171-452A-56</td> <td>Sequence 56, Appl</td>	US-10-171-452A-56	Sequence 56, Appl
41 <td>1030<td>90.6</td><td>238</td><td>12<td>US-10-384-933-54</td><td>Sequence 54, Appl</td></td></td>	1030 <td>90.6</td> <td>238</td> <td>12<td>US-10-384-933-54</td><td>Sequence 54, Appl</td></td>	90.6	238	12 <td>US-10-384-933-54</td> <td>Sequence 54, Appl</td>	US-10-384-933-54	Sequence 54, Appl
42 <td>1030<td>90.6</td><td>238</td><td>15<td>US-10-216-484-54</td><td>Sequence 54, Appl</td></td></td>	1030 <td>90.6</td> <td>238</td> <td>15<td>US-10-216-484-54</td><td>Sequence 54, Appl</td></td>	90.6	238	15 <td>US-10-216-484-54</td> <td>Sequence 54, Appl</td>	US-10-216-484-54	Sequence 54, Appl
43 <td>1029<td>90.5</td><td>236</td><td>10<td>US-09-859-053-30</td><td>Sequence 30, Appl</td></td></td>	1029 <td>90.5</td> <td>236</td> <td>10<td>US-09-859-053-30</td><td>Sequence 30, Appl</td></td>	90.5	236	10 <td>US-09-859-053-30</td> <td>Sequence 30, Appl</td>	US-09-859-053-30	Sequence 30, Appl
44 <td>1028</td> <td>90.5</td> <td>241</td> <td>15<td>US-10-221-945-1</td><td>Sequence 1, Appl</td></td>	1028	90.5	241	15 <td>US-10-221-945-1</td> <td>Sequence 1, Appl</td>	US-10-221-945-1	Sequence 1, Appl
45 <td>1025<td>90.1</td><td>237</td><td>9<td>US-09-056-1608-100</td><td>Sequence 100, App</td></td></td>	1025 <td>90.1</td> <td>237</td> <td>9<td>US-09-056-1608-100</td><td>Sequence 100, App</td></td>	90.1	237	9 <td>US-09-056-1608-100</td> <td>Sequence 100, App</td>	US-09-056-1608-100	Sequence 100, App

ALIGNMENTS

RESULT 1
US-09-917-410-2
; Sequence 2, Application US/09917410
; Patent No. US20020098183A1
GENERAL INFORMATION:

APPLICANT: MARTIN, Ulrich; HASELBECK, Anton; SCHUMACHER, Guenther;
CO, Man S.

TITLE OF INVENTION: ANTI-I-SELECTIN ANTIBODIES FOR PREVENTION OF
MULTIPLE ORGAN FAILURE AFTER POLYTRAUMA AND FOR
PREVENTION OF ACUTE ORGAN DAMAGE AFTER
EXTRACORPOREAL BLOOD CIRCULATION

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Felte & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: U.S.A.

ZIP: 10022

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Computer Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII, WordPerfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/917,410

FILING DATE: 26-Jul-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/578,953

FILING DATE: <Unknown>

APPLICATION NUMBER: EP 95 114 969.9

ATTORNEY/AGENT INFORMATION:

NAME: Hanson, No. US20020098183A1man D.

REGISTRATION NUMBER: 30,946

REFERENCE/DOCKET NUMBER: BOER 1059-PFF/NDH/SLH

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 218
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-917-410-2

Query Match 100.0%; Score 1137; DB 9; Length 218;
Best Local Similarity 100.0%; Pred. No. 4.5e-72;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQWTQSPSSLSASVGRVITTCASQSVYDGDGSYNNWYQKRGKAPKLLIYAASNLES 60
DB 1 DIQWTQSPSSLSASVGRVITTCASQSVYDGDGSYNNWYQKRGKAPKLLIYAASNLES 60
QY 61 GIPSRFSGSGSGTDFLTITSSLOPEDPATYTCQOSNEDPMTFGQGTVEIKRTVAAPSVF 120
DB 61 GIPSRFSGSGSGTDFLTITSSLOPEDPATYTCQOSNEDPMTFGQGTVEIKRTVAAPSVF 120
QY 121 IFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSITYSL 180
DB 121 IFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSITYSL 180
QY 121 IFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSITYSL 180
DB 121 IFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSITYSL 180
QY 181 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 218
DB 181 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 2
US-10-384-933-131
Sequence 131, Application US/10384933
Publication No. US20030170817A1
GENERAL INFORMATION:
APPLICANT: Serizawa, No. US20030170817A1ufusa
APPLICANT: Haruyama, Hideyuki
APPLICANT: Nakahara, Kaori
APPLICANT: Takahashi, Ikuko
APPLICANT: Takahashi, Tohru
TITLE OF INVENTION: Anti-Fas Antibodies
FILE REFERENCE: 980126CIP/HG
CURRENT APPLICATION NUMBER: US/10/384,933
CURRENT FILING DATE: 2003-02-05
PRIOR FILING DATE: 2000-02-09
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/053,583
PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-01
NUMBER OF SEQ ID NOS: 165
SEQ ID NO 131
LENGTH: 238
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Designed light
OTHER INFORMATION: chain of humanized anti-Fas antibody
US-10-384-933-131

Query Match 97.9%; Score 1113; DB 12; Length 238;
Best Local Similarity 98.6%; Pred. No. 2.3e-70;
Matches 215; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIQWTQSPSSLSASVGRVITTCASQSVYDGDGSYNNWYQKRGKAPKLLIYAASNLES 60
DB 21 DIQWTQSPSSLSASVGRVITTCASQSVYDGDGSYNNWYQKRGKAPKLLIYAASNLES 80
QY 61 GIPSRFSGSGSGTDFLTITSSLOPEDPATYTCQOSNEDPMTFGQGTVEIKRTVAAPSVF 120
DB 61 GIPSRFSGSGSGTDFLTITSSLOPEDPATYTCQOSNEDPMTFGQGTVEIKRTVAAPSVF 140

QY 121 IFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSITYSL 180
DB 141 IFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSITYSL 200
QY 181 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 218
DB 201 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238

RESULT 3
US-10-216-484-131
Sequence 131, Application US/10216484
Publication No. US20030103976A1
GENERAL INFORMATION:
APPLICANT: Serizawa, No. US20030103976A1ufusa
APPLICANT: Haruyama, Hideyuki
APPLICANT: Nakahara, Kaori
APPLICANT: Takahashi, Tohru
TITLE OF INVENTION: Anti-Fas Antibodies
FILE REFERENCE: 980126CIP/HG
CURRENT APPLICATION NUMBER: US/10/216,484
CURRENT FILING DATE: 2002-08-09
PRIOR FILING DATE: 2000-02-09
PRIOR APPLICATION NUMBER: US 09/499,662
PRIOR FILING DATE: 2000-02-09
PRIOR APPLICATION NUMBER: US 09/053,583
PRIOR FILING DATE: 1998-04-01
NUMBER OF SEQ ID NOS: 165
SEQ ID NO 131
LENGTH: 238
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Designed light
OTHER INFORMATION: chain of humanized anti-Fas antibody
US-10-216-484-131

Query Match 97.9%; Score 1113; DB 15; Length 238;
Best Local Similarity 98.6%; Pred. No. 2.3e-70;
Matches 215; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIQWTQSPSSLSASVGRVITTCASQSVYDGDGSYNNWYQKRGKAPKLLIYAASNLES 60
DB 21 DIQWTQSPSSLSASVGRVITTCASQSVYDGDGSYNNWYQKRGKAPKLLIYAASNLES 80
QY 61 GIPSRFSGSGSGTDFLTITSSLOPEDPATYTCQOSNEDPMTFGQGTVEIKRTVAAPSVF 120
DB 81 GIPSRFSGSGSGTDFLTITSSLOPEDPATYTCQOSNEDPMTFGQGTVEIKRTVAAPSVF 140
QY 121 IFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSITYSL 180
DB 141 IFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSITYSL 200
QY 181 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 218
DB 201 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238

RESULT 4
US-10-384-933-127
Sequence 127, Application US/10384933
Publication No. US20030170817A1
GENERAL INFORMATION:
APPLICANT: Serizawa, No. US20030170817A1ufusa
APPLICANT: Haruyama, Hideyuki
APPLICANT: Nakahara, Kaori
APPLICANT: Takahashi, Ikuko
APPLICANT: Takahashi, Tohru
TITLE OF INVENTION: Anti-Fas Antibodies
FILE REFERENCE: 980126CIP/HG
CURRENT APPLICATION NUMBER: US/10/384,933
CURRENT FILING DATE: 2003-02-05
PRIOR APPLICATION NUMBER: US/09/499,662

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 31, 2003, 10:29:11 ; Search time 8.20166 Seconds

(without alignments)
1124.623 Million cell updates/sec

Title: US-09-917-410-2

Perfect score: 1137
Sequence: 1 DIQMSPSPSLASVGDRT.....EYTHGLSSPYTKSPKRGEC 218

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 4231058 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/prodata/1/iaa/5A.COMB.pep.*
- 2: /cgn2_6/prodata/1/iaa/5B.COMB.pep.*
- 3: /cgn2_6/prodata/1/iaa/6A.COMB.pep.*
- 4: /cgn2_6/prodata/1/iaa/6B.COMB.pep.*
- 5: /cgn2_6/prodata/1/iaa/PCUS.COMB.pep.*
- 6: /cgn2_6/prodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1137	100.0	218	5	PCT-US96-13152-2
2	1108	97.4	218	2	US-08-887-352B-13
3	1108	97.4	218	3	US-08-466-151-9
4	1108	97.4	218	3	US-09-109-207C-13
5	1108	97.4	218	3	US-09-296-005-13
6	1108	97.4	218	4	US-08-466-163B-9
7	1085	95.4	218	3	US-09-282-505-1
8	1085	95.4	218	3	US-09-054-255-1
9	1085	95.4	218	4	US-09-282-846-1
10	1085	95.4	218	4	US-09-680-145-1
11	1082	95.2	218	2	US-08-887-352B-15
12	1082	95.2	218	2	US-08-887-352B-17
13	1082	95.2	218	2	US-08-887-352B-19
14	1082	95.2	218	2	US-08-887-352B-24
15	1082	95.2	218	3	US-09-109-207C-15
16	1082	95.2	218	3	US-09-109-207C-17
17	1082	95.2	218	3	US-09-109-207C-19
18	1082	95.2	218	3	US-09-109-207C-24
19	1082	95.2	218	3	US-09-296-005-15
20	1082	95.2	218	3	US-09-296-005-17
21	1082	95.2	218	3	US-09-296-005-19
22	1082	95.2	218	3	US-09-296-005-24
23	1026	90.2	214	2	US-07-934-373C-39
24	1026	90.2	214	3	US-08-437-642B-39
25	1026	90.2	214	5	PCT-US93-07832-39
26	1021	89.8	214	2	US-07-934-373C-40
27	1021	89.8	214	2	US-08-788-800-11

28	1021	89.8	214	3	US-08-437-642B-40	Sequence 40, Appl
29	1021	89.8	214	3	US-09-097-309-2	Sequence 2, Appl
30	1021	89.8	214	3	US-09-097-171A-2	Sequence 2, Appl
31	1021	89.8	214	4	US-09-460-587-2	Sequence 2, Appl
32	1021	89.8	214	5	PCT-US93-07832-40	Sequence 40, Appl
33	1021	89.8	214	5	US-07-934-373C-25	Sequence 25, Appl
34	1021	89.8	214	3	US-08-437-642B-25	Sequence 25, Appl
35	1021	89.8	214	4	US-08-146-206C-25	Sequence 25, Appl
36	1021	89.8	214	5	PCT-US93-07832-25	Sequence 25, Appl
37	1021	89.8	214	3	US-09-097-309-6	Sequence 6, Appl
38	1021	89.8	214	3	US-09-097-171A-10	Sequence 10, Appl
39	1021	89.8	214	3	US-09-422-712B-2	Sequence 2, Appl
40	1021	89.8	214	3	US-09-607-756-2	Sequence 2, Appl
41	1021	89.8	214	4	US-09-460-587-6	Sequence 6, Appl
42	1021	89.8	214	4	US-09-740-002-24	Sequence 24, Appl
43	1019.5	89.7	242	3	US-09-027-449-62	Sequence 62, Appl
44	1019.5	89.7	242	3	US-09-026-985-62	Sequence 62, Appl
45	1019.5	89.7	242	4	US-09-121-952A-62	Sequence 62, Appl

ALIGNMENTS

RESULT 1
PCT-US96-13152-2
Sequence 2, Application PC/TUS9613152
GENERAL INFORMATION:
APPLICANT: Martin, Ulrich, et al.
TITLE OF INVENTION: Anti-selectin antibodies for prevention of multiple organ fai
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felte & Lynch
ADDRESSEE: Attn: Norman D. Hanson
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Computer Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/13152
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/578,953
FILING DATE: 27-Dec-95
APPLICATION NUMBER: EP 95 112 895.8
FILING DATE: 17-Aug-95
APPLICATION NUMBER: EP 95 114 969.9
FILING DATE: 19-Sep-95
ATTORNEY/AGENT INFORMATION:
NAME: Norman D. Hanson
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: BOER 1059-PCT-PFF/NDH
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 218
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-13152-2
Query Match 100.0%; Score 1137; DB 5; Length 218;
Best Local Similarity 100.0%; Pred. No. 1.5e-87; Indels 0; Gaps 0;
Matches 218; Conservative 0; Mismatches 0;

QY 1 DIQMTQSPSSLSASVGRVTTITCKASQSVVDYDGSYNNMWYQKPKKLIYAASNL60
DB 1 DIQMTQSPSSLSASVGRVTTITCKASQSVVDYDGSYNNMWYQKPKKLIYAASNL60
QY 61 GIPRFGSGSGGTFTLTITSLQPEDPATYTCQOSNEDPMTFGGTKEIKRTVAAPS6V 120
DB 61 GIPRFGSGSGGTFTLTITSLQPEDPATYTCQOSNEDPMTFGGTKEIKRTVAAPS6V 120
QY 121 IFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKOSTYSL6 180
DB 121 IFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKOSTYSL6 180
QY 181 STLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC 218
DB 181 STLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC 218

RESULT 2
US-08-887-352B-13
Sequence 13, Application US/08887352B
Patent No. 5994511
GENERAL INFORMATION:
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardiou, John Lowe
TITLE OF INVENTION: Improved Anti-IgG Antibodies and Method of
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,352B
FILING DATE: 03-Jul-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P1123
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 218 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-887-352B-13

Query Match 97.4%; Score 1108; DB 2; Length 218;
Best Local Similarity 97.2%; Pred. No. 4e-85; 1; Indels 0; Gaps 0;
Matches 212; Conservative 5; Mismatches 1;

QY 1 DIQMTQSPSSLSASVGRVTTITCKASQSVVDYDGSYNNMWYQKPKKLIYAASNL60
DB 1 DIQMTQSPSSLSASVGRVTTITCKASQSVVDYDGSYNNMWYQKPKKLIYAASNL60
QY 61 GIPRFGSGSGGTFTLTITSLQPEDPATYTCQOSNEDPMTFGGTKEIKRTVAAPS6V 120
DB 61 GIPRFGSGSGGTFTLTITSLQPEDPATYTCQOSNEDPMTFGGTKEIKRTVAAPS6V 120
QY 121 IFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKOSTYSL6 180
DB 121 IFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKOSTYSL6 180

QY 181 STLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC 218
DB 181 STLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC 218

RESULT 3
US-08-466-151-9
Sequence 9, Application US/08466151
Patent No. 6037453
GENERAL INFORMATION:
APPLICANT: Jardiou, Paula M.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,151
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/466163
FILING DATE: 06-Jun-1995
APPLICATION NUMBER: 08/405617
FILING DATE: 15-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/185899
FILING DATE: 26-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/879495
FILING DATE: 07-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/744768
FILING DATE: 14-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P0718P2C1D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 218 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-466-151-9

Query Match 97.4%; Score 1108; DB 3; Length 218;
Best Local Similarity 97.2%; Pred. No. 4e-85; 1; Indels 0; Gaps 0;
Matches 212; Conservative 5; Mismatches 1;

QY 1 DIQMTQSPSSLSASVGRVTTITCKASQSVVDYDGSYNNMWYQKPKKLIYAASNL60
DB 1 DIQMTQSPSSLSASVGRVTTITCKASQSVVDYDGSYNNMWYQKPKKLIYAASNL60
QY 61 GIPRFGSGSGGTFTLTITSLQPEDPATYTCQOSNEDPMTFGGTKEIKRTVAAPS6V 120
DB 61 GIPRFGSGSGGTFTLTITSLQPEDPATYTCQOSNEDPMTFGGTKEIKRTVAAPS6V 120
QY 121 IFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKOSTYSL6 180
DB 121 IFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKOSTYSL6 180

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 31, 2003, 10:29:11 ; Search time 17 Seconds

(without alignments)
2506.043 Million cell updates/sec

Title: US-09-917-410-4

Perfect score: 2357
Sequence: 1 EVQLVDSGGGLVPGGSLRL.....MREAALNHTYQKSLISLQK 443

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 9616862 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: PIR 76:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1743	73.9	327	1 G4HU	Ig gamma-4 chain C
2	1605.5	68.1	326	1 G2HU	Ig gamma-2 chain C
3	1590.5	67.5	330	1 GHU	Ig gamma-1 chain C
4	1585	67.2	377	2 A60764	Ig gamma-3 chain C
5	1575	66.8	377	2 A23511	Ig gamma-3 chain C
6	1519	64.4	470	2 S22080	Ig heavy chain pre
7	1495.5	63.4	444	2 PC4436	monoclonal antibod
8	1454	61.7	472	2 S31459	Ig gamma-1 chain -
9	1422.5	60.4	469	2 S37483	Ig gamma-2a chain
10	1417	60.1	446	2 S40295	Ig gamma-2a chain
11	1384	58.7	474	1 G2MS11	Ig gamma-2b chain
12	1348	57.2	374	2 S69339	Ig heavy chain V r
13	1331.5	56.5	475	2 S01321	Ig gamma-2b chain
14	1289.5	54.7	328	2 I47159	Ig gamma-2a chain
15	1283.5	54.5	328	2 I47160	Ig gamma-2b chain
16	1264.5	53.6	328	2 I47161	Ig gamma-2b chain
17	1240.5	52.6	328	2 I47158	Ig gamma-3 chain C
18	1199	50.9	323	1 GHRB	Ig gamma-1 chain C
19	1162	49.3	329	1 G2GP	Ig gamma-2 chain C
20	1147	48.7	308	2 C30554	Ig heavy chain C r
21	1139.5	48.3	255	4 S31866	Ig gamma-1 chain C
22	1129.5	47.9	234	2 P70207	Ig gamma chain C r
23	1124	47.7	333	2 PS0018	Ig gamma-2b chain
24	1118.5	47.5	326	2 PS0017	Ig gamma-1 chain C
25	1108.5	47.0	289	1 G3HUM1	Ig gamma-3 heavy C
26	1108	47.0	329	2 S00847	Ig gamma-2c chain
27	1106.5	46.9	324	1 G1MS	Ig gamma-1 chain C
28	1106.5	46.9	330	1 G2MSA	Ig gamma-2a chain
29	1104	46.8	548	2 S38864	Ig epsilon chain C

30	1103	46.8	327	2 S06611	Ig gamma-2 chain C
31	1101.5	46.7	393	1 G1MS	Ig gamma-1 chain C
32	1101.5	46.7	399	1 G2MSAM	Ig gamma-2a chain
33	1099	46.6	335	1 G2MSAB	Ig gamma-2a chain
34	1098.5	46.6	329	1 G3MSC	Ig gamma-3 chain C
35	1090.5	46.3	398	1 G3MSM	Ig gamma-3 chain C
36	1085.5	46.1	277	2 I47162	Ig gamma-4 chain C
37	1084.5	46.0	322	2 PS0019	Ig gamma-2a chain
38	1049.5	44.5	505	1 G2MSBM	Ig gamma-2b chain
39	899.5	38.2	249	2 S04845	Ig heavy chain pre
40	872.5	37.0	249	2 S69340	Ig heavy chain VHI
41	861.5	36.6	572	2 B46529	Ig y heavy chain (
42	825.5	35.0	241	2 S69331	Ig heavy chain (DO
43	805	34.2	218	2 A36040	Ig heavy chain V-I
44	768.5	32.6	220	2 A49444	Ig gamma-1 heavy C
45	767	32.5	627	2 S14683	Ig mu chain precur

ALIGNMENTS

RESULT 1

G4HU

Ig gamma-4 chain C region - human

C/Species: Homo sapiens (man)

C/Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #ext_change 16-Jul-1999

C/Accession: A90933; A90249; A02150

R/Ellison, J.; Buxbaum, J.; Hood, L.

DNA 1, 11-18, 1981

A/Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.

A/Reference number: A90933; PMID:83157104; PMID:6299662

A/Accession: A90933

A/Molecule type: DNA

A/Residues: 1-327 <EL>

A/Note: the sequence was determined from the germline gene

R/Pink, J.R.L., Buttery, S.H.; De Vries, G.M.; Milstein, C.

Biochem. J. 117, 33-47, 1970

A/Title: Human immunoglobulin subclasses. Partial amino acid sequence of the constant

A/Reference number: A90249; PMID:70207560; PMID:4192699

A/Accession: A90249

A/Molecule type: protein

A/Residues: 1-30,81-326 <PIN>

C/Genetics:

A/Gene: GDB:IGHG4

A/Cross-references: GDB:119340; OMIM:147130

A/Map position: 14q32.33-14q32.33

A/Introns: 99/1; 111/1; 221/1

C/Complex: An immunoglobulin heterotrimer subunit consists of two identical light (kappa)

C/Superfamily: immunoglobulin C region; immunoglobulin homology

C/Keywords: duplication; glycoprotein; heterotrimer; immunoglobulin

F:20-85/Domain: immunoglobulin homology <IM1>

F:99-110/Region: hinge

F:134-203/Domain: immunoglobulin homology <IM2>

F:240-307/Domain: immunoglobulin homology <IM3>

F:4/Dsulfide bonds: interchain (to light chain) #status experimental

F:27-83,141-201,247-305/Dsulfide bonds: #status predicted

F:106,109/Dsulfide bonds: interchain (to heavy chain) #status experimental

F:177/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 73.9%; Score 1743; DB 1; Length 327;

Best Local Similarity 100.0%; Pred. No. 1.2e-93;

Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	117	ASTKGSVPPLAPCGSTSESTRALGCVKDYPPPEVTYSNMSGALITSGVHTFPALQSS	176
DB	1	ASTKGSVPPLAPCGSTSESTRALGCVKDYPPPEVTYSNMSGALITSGVHTFPALQSS	60
QY	177	GLYSLSSVTVTPSSSLGTITTCNVDRKPSNTRKVDGRVSKYGPCCPSCPAPFLGSPV	236
DB	61	GLYSLSSVTVTPSSSLGTITTCNVDRKPSNTRKVDGRVSKYGPCCPSCPAPFLGSPV	120
QY	237	PLFPKPKDTLMTISRTPEVTCVVVDVSDPEVDQFNWYVDGVEVHNAKTKRPREEQNSTY	296

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Db      121  FLPPKPKDLMISRTPEVTCVVVDVSDPEDEVDFNMVVDVEVHNATKPRERQFNSTY 180
      297  RVSVVLTVLHODMNGEKYCKVKSNKGLPSSIEKTIISAKAGQPREPOVYTLPPSQEEMTK 356
      181  RVSVVLTVLHODMNGEKYCKVKSNKGLPSSIEKTIISAKAGQPREPOVYTLPPSQEEMTK 240
      357  NVSVLTVLVKGFYPSDIAVWESNGQPENNYKTPPVLDSDGSFFLYSRLTVDRSRMQEG 416
      241  NVSVLTVLVKGFYPSDIAVWESNGQPENNYKTPPVLDSDGSFFLYSRLTVDRSRMQEG 300
      417  NVFSCSVWHEALHNHYTQKSLSLSTCK 443
      301  NVFSCSVWHEALHNHYTQKSLSLSTCK 327

RESULT 2
GHU
IG gamma-2 chain C region - human
C/Species: Homo sapiens (man)
C/Date: 30-Apr-1991 #sequence revision 13-Jun-1993 #text_change 21-Jul-2000
C/Accession: A93906; A92809; A90752; A93132; A02148
R:Ellison, J.; Hood, L. U.S.A. 79, 1984-1988, 1982
A/Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain c
A/Reference number: A93906; MUID:82197621; PMID:6804948
A/Accession: A93906
A/Molecule type: DNA
A/Residues: 1-326 <ELL>
A/Cross-references: GB:V00554; GB:J00230; NID:932759; PIDN:CB58438.1; PID:ig6066056
R/Note: Lys-326 is probably removed posttranslationally
R/Wang, A.C.; Tung, E.; Fudenberg, H.H.
J. Immunol. 125, 1048-1054, 1980
A/Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and f
A/Reference number: A92809; MUID:81007873; PMID:6774012
A/Accession: A92809
A/Contents: myeloma protein T11
A/Molecule type: protein
A/Residues: 1-19, 'Q', 21-57, 'Z', 59, 'A', 61-193, 'D', 195-325 <WAN>
R/Note: Trp-156 is at or near the complement-binding site
R/Connell, G.E.; Parr, D.M.; Hofmann, T.
Can. J. Biochem. 57, 758-767, 1979
A/Title: The amino acid sequences of the three heavy chain constant region domains of a
A/Reference number: A90752; MUID:80001357; PMID:113060
A/Accession: A90752
A/Contents: myeloma protein Zie
A/Molecule type: protein
A/Residues: 1-24, 'E', 26-57, 'EV', 60-85, 132-171, 'ZZZ', 175, 'B', 177-193, 'D', 195-196, 'Q', 198-
A/Note: this sequence has since been revised
R/Hofmann, T.; Parr, D.M.
Mol. Immunol. 16, 923-925, 1979
A/Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin g
A/Reference number: A93132; MUID:80114419; PMID:118920
A/Accession: A93132
A/Contents: Zie
A/Molecule type: protein
A/Residues: 238-275 <HOF>
R/Hofmann, T.; Parr, D.M.
submitted to the Atlas, March 1980
A/Reference number: A94591
A/Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268
A/Note: the revised sequence differs from that shown in having 60-Ala and in the amidat
ned
R/Milstein, C.; Frangione, B.
Biochem. J. 121, 217-225, 1971
A/Title: Disulfide bridges of the heavy chain of human immunoglobulin G2.
A/Reference number: A90253; MUID:72033500; PMID:4940472
A/Contents: annotation; myeloma protein Sa, disulfide bonds
R/Frangione, B.; Milstein, C.; Pink, J.R.L.
Nature 221, 145-148, 1969
A/Title: Structural studies of immunoglobulin G.
A/Reference number: A93157; MUID:69064124; PMID:5782707
A/Contents: annotation; Sa, disulfide bonds

```

```

C/Genetics:
A/Gene: GDB:119338; OMIM:147110
A/Cross-references: GDB:119338; OMIM:147110
A/Map position: 14q32.33-14q32.33
C/Complex: An immunoglobulin heterotrimer subunit consists of two identical light (ka)
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1
C/Superfamily: Immunoglobulin C region; immunoglobulin homology
C/Keywords: duplication; glycoprotein; heterotrimer; immunoglobulin
F/20-85/Domain: immunoglobulin homology <IM>
F/133-202/Domain: immunoglobulin homology <IM2>
F/239-306/Domain: immunoglobulin homology <IM3>
F/14/Disulfide bonds: interchain (to light chain) #status experimental
F/27-83,140-200,246-304/Disulfide bonds: #status experimental
F/102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F/176/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match      68.1%; Score 1605.5; DB 1; Length 326;
Best Local Similarity 92.4%; Pred. No. 1e-85;
Matches 302; Conservative 10; Mismatches 14; Indels 1; Gaps 1;

Db      117  ASTKGPVFPFLAPCSRSTSESTALGCLVDYDPEPVTVSMNSGALTSGVHTPPAVLQSS 176
      1  ASTKGPVFPFLAPCSRSTSESTALGCLVDYDPEPVTVSMNSGALTSGVHTPPAVLQSS 60
      177  GLVSLSSVTVTPSSSUGTKTYTCNVDRKPSNTVDKRVESKYGPPCPSCPAPEFLGSPV 236
      61  GLVSLSSVTVTPSSNFQTYTCNVDRKPSNTVDKRVESKYGPPCPSCPAPEFLGSPV 119
      237  FLPPKPKDLMISRTPEVTCVVVDVSDPEDEVDFNMVVDVEVHNATKPRERQFNSTY 296
      120  FLPPKPKDLMISRTPEVTCVVVDVSDPEDEVDFNMVVDVEVHNATKPRERQFNSTY 179
      297  RVSVVLTVLHODMNGEKYCKVKSNKGLPSSIEKTIISAKAGQPREPOVYTLPPSQEEMTK 356
      180  RVSVVLTVLHODMNGEKYCKVKSNKGLPSSIEKTIISAKAGQPREPOVYTLPPSQEEMTK 239
      357  NVSVLTVLVKGFYPSDIAVWESNGQPENNYKTPPVLDSDGSFFLYSRLTVDRSRMQEG 416
      241  NVSVLTVLVKGFYPSDIAVWESNGQPENNYKTPPVLDSDGSFFLYSRLTVDRSRMQEG 299
      417  NVFSCSVWHEALHNHYTQKSLSLSTCK 443
      300  NVFSCSVWHEALHNHYTQKSLSLSTCK 326

RESULT 3
GHU
IG gamma-1 chain C region - human
C/Species: Homo sapiens (man)
C/Date: 31-Jan-1981 #sequence revision 18-Aug-1982 #text_change 16-Jul-1999
C/Accession: A93433; S36861; S33887; B90563; A90564; B91668; A91723; A02146
R:Ellison, J.W.; Beron, B.J.; Hood, L.E.
Nucleic Acids Res. 10, 4071-4079, 1982
A/Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.
A/Reference number: A93433; MUID:82274238; PMID:6287432
A/Accession: A93433
A/Molecule type: DNA
A/Residues: 1-330 <ELL>
A/Cross-references: EMBL:Z17370
A/Note: this sequence has the Gln(17) alleotypic marker, 97-Lys, and the Gln(1) markers,
R/Harris, L.J.
submitted to the EMBL Data Library, October 1992
A/Reference number: S33904
A/Accession: S36861
A/Molecule type: DNA
A/Residues: 2-330 <HAR>
A/Cross-references: EMBL:Z17370
R:Takahashi, N.; Ueda, S.; Obata, M.; Nikaide, T.; Nakai, S.; Honjo, T.
Cell 29, 671-679, 1982
A/Title: Structure of human immunoglobulin gamma genes: implications for evolution of e
A/Reference number: S33887; MUID:83001943; PMID:6811139
A/Accession: S33887

```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 31, 2003, 10:29:10 ; Search time 10.6667 Seconds

(without alignments)
1953.078 Million cell updates/sec

Title: US-09-917-410-4

Perfect score: 2357

Sequence: 1 EVOLVESGGGLVPGGSLRL.....MPEALNHTYQKSLSLGK 443

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 segs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1743	73.9	327	1 GC4_HUMAN	P01861 homo sapien
2	1605.5	68.1	326	1 GC2_HUMAN	P01859 homo sapien
3	1590.5	67.5	330	1 GC1_HUMAN	P01857 homo sapien
4	1199	50.9	323	1 GC_RABIT	P01870 oryctolagus
5	1162	49.3	329	1 GC2_CAVPO	P01862 cavia porce
6	1124	47.7	333	1 GC2_CAVPO	P01861 cavia porce
7	1118.5	47.5	326	1 GC1_RAT	P01860 ratu
8	1113.5	47.2	290	1 GC3_HUMAN	P01860 homo sapien
9	1108	47.0	329	1 GC3_RAT	P20762 ratu
10	1106.5	46.9	324	1 GC1_MOUSE	P01868 mus musculu
11	1106.5	46.9	330	1 GC1_MOUSE	P01868 mus musculu
12	1101.5	46.7	393	1 GC1_MOUSE	P01869 mus musculu
13	1101.5	46.7	399	1 GC1_MOUSE	P01869 mus musculu
14	1099	46.6	335	1 GCAB_MOUSE	P01864 mus musculu
15	1098.5	46.6	329	1 GC3_MOUSE	P22436 mus musculu
16	1090.5	46.3	398	1 GC3_MOUSE	P03987 mus musculu
17	1084.5	46.0	322	1 GC1_RAT	P20760 ratu
18	1054.5	44.7	336	1 GCB_MOUSE	P01866 mus musculu
19	1049.5	44.5	405	1 GCB_MOUSE	P01867 mus musculu
20	496	21.0	429	1 EPC_RAT	P01855 ratu
21	482.5	20.5	421	1 EPC_MOUSE	P06336 mus musculu
22	478.5	20.3	428	1 EPC_HUMAN	P01858 homo sapien
23	478	20.3	122	1 HV3G_HUMAN	P01768 homo sapien
24	463.5	19.7	121	1 HV3J_HUMAN	P01771 homo sapien
25	462.5	19.6	117	1 HV3C_HUMAN	P01764 homo sapien
26	459	19.3	136	1 HV16_MOUSE	P01783 mus musculu
27	454.5	19.3	120	1 HV3E_HUMAN	P01766 homo sapien
28	454	19.3	116	1 HV3T_HUMAN	P01766 homo sapien
29	451	19.1	114	1 HV3B_HUMAN	P01767 homo sapien
30	450.5	19.1	115	1 HV3F_HUMAN	P01767 homo sapien
31	449.5	19.1	115	1 HV3D_HUMAN	P01765 homo sapien
32	447.5	19.0	454	1 MUC_HUMAN	P01871 homo sapien
33	447	19.0	455	1 MUC_MOUSE	P01872 mus musculu

34	446	18.9	97	1 HV56_MOUSE	P18527 mus musculu
35	443.5	18.8	117	1 HV02_CANFA	P01785 canis fami
36	443	18.8	116	1 HV05_CARAU	P19181 carassius a
37	441	18.7	126	1 HV3K_HUMAN	P01772 homo sapien
38	440.5	18.7	119	1 HV3I_HUMAN	P01770 homo sapien
39	438	18.6	119	1 HV3J_MOUSE	P01807 mus musculu
40	438	18.6	119	1 HV3E_MOUSE	P01808 mus musculu
41	438	18.6	122	1 HV3H_HUMAN	P01769 homo sapien
42	437	18.5	476	1 MUC_MOUSE	P01873 mus musculu
43	435	18.5	119	1 HV3M_HUMAN	P01774 homo sapien
44	433.5	18.4	118	1 HV39_MOUSE	P01809 mus musculu
45	433.5	18.4	457	1 MUC_SUNMU	P20768 sunco mur

ALIGNMENTS

RESULT 1					
GC4_HUMAN	STANDARD;	PRT;	327 AA.		
AC	P01861;				
DT	21-JUL-1986 (Rel. 01, Created)				
DT	21-JUL-1986 (Rel. 01, Last sequence update)				
DT	15-SEP-2003 (Rel. 42, Last annotation update)				
DE	IG gamma-4 chain C region.				
GN	IGHG4.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=83157104; PubMed=6299662;				
RA	Edlison J.W., Buxbaum J.N., Hood L.E.;				
RT	"Nucleotide sequence of a human immunoglobulin C gamma 4 gene.";				
RL	DNA 1:11-18(1981).				
RN	[2]				
RP	SEQUENCE OF 1-30 AND 81-326.				
RX	MEDLINE=70207560; PubMed=4192699;				
RA	Pink J.R.L., Buttery S.H., de Vries G.M., Milstein C.;				
RT	"Human immunoglobulin subclasses. Partial amino acid sequence of the				
RL	Biochem. J. 117:33-47(1970).				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -				
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CC	or send an email to license@isb-sib.ch).				
CC	-----				
DR	EMBL; K01316; AAB59394.1; ALT_INIT.				
DR	PIR; A90933; GAHU.				
DR	PDB; 1ADQ; 16-SEP-98.				
DR	Genew; HGNC:5528; IGHG4.				
DR	MIM; 147130; -				
DR	GO; GO:0005624; C:membrane fraction; NMS.				
DR	GO; GO:0008233; F:antigen binding activity; TAS.				
DR	GO; GO:0006955; P:immune response; NMS.				
DR	InterPro; IPR007110; IG-like.				
DR	InterPro; IPR003597; IG_c1.				
DR	InterPro; IPR003006; IG_MHC.				
DR	Pfam; PF00047; IG_3.				
DR	SMART; SM00407; IGH1; 2.				
DR	PROSITE; PSS0835; IG_LIKE; 3.				
DR	PROSITE; PSS0290; IG_MHC; 2.				
KM	Immunoglobulin domain; Immunoglobulin C region; 3D-structure.				
FT	NON TER	1	98		CH1.
FT	DOMAIN	99	110		HINGE.
FT	DOMAIN	111	220		CH2.
FT	DOMAIN	221	327		CH3.

Query Match 327: Conservative 73.9%; Score 1743; DB 1; Length 327;
 Best Local Similarity 100.0%; Pred. No. 2e-114;
 Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

FT DISULFID 14 14 INTERCHAIN (WITH A LIGHT CHAIN).
 FT DISULFID 27 83
 FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 141 201
 FT DISULFID 247 305
 SQ SEQUENCE 327 AA; 35940 MW; 3EDBD11EF208E7A CRC64;

Query 117 ASTGSPVFPPLAPCRSTSESTALGCLVXYFPEPVVSNMGLTSGVTFPPVLDSS 176
 Db 1 ASTGSPVFPPLAPCRSTSESTALGCLVXYFPEPVVSNMGLTSGVTFPPVLDSS 60

Query 177 GLYSLSVVTVPSSSLGRTKTYTCNVDRHKPSMTKVDRVSKYKGPCCPAPDFLGGPSV 236
 Db 61 GLYSLSVVTVPSSSLGRTKTYTCNVDRHKPSMTKVDRVSKYKGPCCPAPDFLGGPSV 120

Query 237 FLFPPKPKDTLMISRTPEVTCVVVDVSDGEDEVQFNWYVDGVVNAKTKRREQFSTY 296
 Db 121 FLFPPKPKDTLMISRTPEVTCVVVDVSDGEDEVQFNWYVDGVVNAKTKRREQFSTY 180

Query 297 RVSVTLTVLHODMNLGKSKYKCKVSKGLPSSIEKTIISKAKGPPRPQYTTLPSCQENTK 356
 Db 181 RVSVTLTVLHODMNLGKSKYKCKVSKGLPSSIEKTIISKAKGPPRPQYTTLPSCQENTK 240

Query 357 NOVSLTCLVKGFPSPDIWVEMSNQPPNNYKTPPVLDSSGFLYSRLTVDSKRMQEG 416
 Db 241 NOVSLTCLVKGFPSPDIWVEMSNQPPNNYKTPPVLDSSGFLYSRLTVDSKRMQEG 300

Query 417 NVFSCSVMEHALNHNHYTKSLSLSLGK 443
 Db 301 NVFSCSVMEHALNHNHYTKSLSLSLGK 327

RESULT 2
 GC2_HUMAN STANDARD; PRT; 326 AA.
 AC P01859;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Ig gamma-2 chain C region.
 GN IGHG2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE OF 2-326 FROM N.A.
 RX MEDLINE=82197621; PubMed=6804948;
 RA Ellison J.W., Hood L.E.;
 RT "Linkage and sequence homology of two human immunoglobulin gamma
 RT heavy chain constant region genes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988(1982).
 RN [2]
 RP SEQUENCE OF 88-115 FROM N.A.
 RX MEDLINE=83001943; PubMed=6811139;
 RA Takahashi N., Ueda S., Obata M., Nikiido T., Nakai S., Honjo T.;
 RT "Structure of human immunoglobulin gamma genes: implications for
 RT evolution of a gene family.";
 RL Cell 29:671-679(1982).
 RN [3]
 RP SEQUENCE OF 99-177 AND 310-326 FROM N.A.
 RX MEDLINE=84235992; PubMed=6329676;
 RA Krawinkel U., Rablites T.H.;
 RT "Comparison of the hinge-coding segments in human immunoglobulin gamma
 RT heavy chain genes and the linkage of the gamma 2 and gamma 4 subclasses
 RT genes.";

RL EMBL J. 1:403-407(1982).
 RN [4]
 RP SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL).
 RX MEDLINE=81007873; PubMed=6774012;
 RA Wang A.-C., Tung B., Fudenberg H.H.;
 RT "The primary structure of a human IgG2 heavy chain: genetic,
 RT evolutionary, and functional implications.";
 RL J. Immunol. 125:1048-1054(1980).
 RN [5]
 RP SEQUENCE OF 1-85 AND 132-125 (MYELOMA PROTEIN ZIE).
 RX MEDLINE=80001357; PubMed=113060;
 RA Connell G.E., Parr D.M., Hofmann T.;
 RT "The amino acid sequences of the three heavy chain constant region
 RT domains of a human IgG2 myeloma protein.";
 RL Can. J. Biochem. 57:758-767(1979).
 RN [6]
 RP SEQUENCE OF 238-275 (ZIE).
 RX MEDLINE=80114419; PubMed=118920;
 RA Hofmann T., Parr D.M.;
 RT "A note of the amino acid sequence of residues 381-391 of human
 RT immunoglobulin gamma chains.";
 RL Mol. Immunol. 16:923-925(1979).
 RN [7]
 RP REVISIONS TO 25; 59; 60 AND 264-268 (ZIE).
 RA Hofmann T., Parr D.M.;
 RL Submitted (MAR-1980) to the PIR data bank.
 RN [8]
 RP SEQUENCE OF 1-121 (DOT).
 RX MEDLINE=95255298; PubMed=7737190;
 RA Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;
 RT "Characterization of the two unique human anti-flavin monoclonal
 RT immunoglobulins.";
 RL Eur. J. Biochem. 228:886-893(1995).
 RN [9]
 RP DISULFIDE BONDS.
 RX MEDLINE=72033500; PubMed=4940472;
 RA Milstein C., Frangione B.;
 RT "Disulphide bridges of the heavy chain of human immunoglobulin G2.";
 RL Biochem. J. 121:217-225(1971).
 RN [10]
 RP DISULFIDE BONDS.
 RX MEDLINE=69064124; PubMed=5782707;
 RA Frangione B., Milstein C., Pink U.R.L.;
 RT "Structural studies of immunoglobulin G.";
 RL Nature 221:145-148(1969).
 CC -----
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 CC -----
 DR EMBL J00230; AAB59393.1; -;
 DR PIR; A93906; G2HU.
 DR HSSP; P01857; IFC1.
 DR Genew; HGNC:5526; IGHG2.
 DR MIM; 147110; -;
 DR GO; GO:0005624; C:membrane fraction; NAS.
 DR GO; GO:0003823; F:antigen binding activity; TNS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig cl.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; Ig; 3.
 DR SMART; SM00407; Igcl; 2.
 DR PROSITE; PS00835; Ig_LIKE; 3.
 DR PROSITE; PS00290; IG_MHC; 2.
 KW Immunoglobulin domain; Immunoglobulin C region.
 FT NON TER 1 98 CH1.
 FT DOMAIN 99 110 HINGE.

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OM protein - protein search, using sw model

Run on: December 31, 2003, 10:29:10 ; Search time 37.6667 Seconds

(without alignments)
3034.973 Million cell updates/sec

Title: us-09-917-410-4

Perfect score: 2357 1 EVOLVESGGGLVPGGSLRL.....MEKALNNHTYQKSLSLGK 443

Sequence: 1 EVOLVESGGGLVPGGSLRL.....MEKALNNHTYQKSLSLGK 443

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPREMBL_23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacterioplasmid:*
17: sp_archaeoplasmid:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2091.5	88.7	471	4	08TC77
2	2032	86.2	473	4	08TC63
3	1990.5	84.5	521	4	08N4Y9
4	1571	66.7	509	4	08NFI7
5	1557.5	66.1	469	11	08R3V9
6	1547.5	65.7	437	11	08R1A4
7	1515.5	64.3	473	11	091Z05
8	1471.5	62.4	473	11	09D8L4
9	1458.5	61.9	463	11	0991C4
10	1432	60.8	468	11	0991J1
11	1405.5	59.6	473	11	0991L25
12	1376	58.4	474	11	08R3H6
13	1217	51.6	337	6	095M34
14	1149.5	48.8	701	4	096PQ8
15	967.5	41.0	597	4	096BB9
16	929	39.4	613	4	08WUK1

17	876.5	37.2	487	11	099KA4	099KA4 mus musculu
18	868	36.8	494	4	096K68	096K68 homo sapien
19	852.5	36.2	499	4	08N5K4	08N5K4 homo sapien
20	846.5	35.9	493	4	08NCL6	08NCL6 homo sapien
21	836	35.5	486	11	091Z07	091Z07 mus musculu
22	820.5	34.8	479	11	091WPS	091WPS mus musculu
23	788.5	33.5	480	11	091XEL	091XEL mus musculu
24	772	32.8	484	11	08VEA0	08VEA0 mus musculu
25	764.5	32.4	614	4	096GA6	096GA6 homo sapien
26	758.5	32.2	597	4	09BUI0	09BUI0 homo sapien
27	754	32.0	613	4	096EY0	096EY0 homo sapien
28	752.5	31.9	597	4	09B0B8	09B0B8 homo sapien
29	748.5	31.8	588	4	08WUX4	08WUX4 homo sapien
30	746	31.7	618	4	096FA6	096FA6 homo sapien
31	745	31.8	613	11	08VCX7	08VCX7 mus musculu
32	735	31.2	278	11	0921K1	0921K1 mus musculu
33	724	30.7	482	11	091X92	091X92 mus musculu
34	707	30.0	500	4	09BRV0	09BRV0 homo sapien
35	704	29.9	496	4	096KX8	096KX8 homo sapien
36	701	29.7	573	4	08WU38	08WU38 homo sapien
37	697	29.6	484	11	099LA6	099LA6 mus musculu
38	689.5	29.3	497	4	08WY24	08WY24 homo sapien
39	685	29.1	482	11	08K172	08K172 mus musculu
40	685	29.1	486	4	096DK0	096DK0 mus sapien
41	678	28.8	480	11	08K0Z4	08K0Z4 mus musculu
42	675.5	28.7	481	11	091WT1	091WT1 mus musculu
43	674	28.6	488	11	091WR1	091WR1 mus musculu
44	665.5	28.2	489	11	08VCX4	08VCX4 mus musculu
45	665	28.2	488	11	08K0F2	08K0F2 mus musculu

ALIGNMENTS

RESULT 1	08TC77	PRELIMINARY;	PRT;	471 AA.
AC	08TC77;			
DT	01-JUN-2002 (TEMBLrel. 21, Created)			
DT	01-JUN-2002 (TEMBLrel. 21, Last sequence update)			
DT	01-MAR-2003 (TEMBLrel. 23, Last annotation update)			
DE	Hypothetical protein.			
OS	Homo sapiens (human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxId=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Splice;			
RA	Strausberg R.;			
RL	Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; BC024289; AAH24289.1; -			
DR	InterPro; IPR007110; IG_11ke.			
DR	InterPro; IPR003006; IG_MHC.			
DR	InterPro; IPR003596; IG_V.			
DR	Pfam; PF00047; IG_4.			
DR	SMART; SM00406; IG_1.			
DR	PROSITE; PSS0835; IG_LIKE; 4.			
DR	PROSITE; PSS00290; IG_MHC; 2.			
KW	Hypothetical protein.			
SQ	SEQUENCE 471 AA; 51791 MW; 388F7F4CF588660E CRC64;			
Query Match	88.7%; Score 2091.5; DB 4; Length 471;			
Best local similarity	88.3%; Pred. No. 8.8e-166;			
Matches	399; Conservative 21; Mismatches 23; Indels 9; Gaps 3;			
QY	1 EVOLVESGGGLVPGGSLRLISCAAGFTSTYAMSVWRQAPGKLEWVASISTGGS-TYY 59			
DB	20 EVOLVESGGGLVPGGSLRLISCAAGFTSTYAMSVWRQAPGKLEWVASISTGGS-TYY 79			
QY	60 PDSVKGRFTISRNANKNTLYLQNSLRABDTAYVYCAKVD-----GYPDYWGQGLTVV 114			
DB	80 ADSVKGRFTISRNANKNTLYLQNSLRABDTAYVYCAKVDRLQTLTSYWFEDLWGRGTLTVV 139			

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QY 115 SSASTKGPVPEPLAPCSRSTSESTALGCLVKDYFPEPVTVSNMGSALTSGVHTFPAVLQ 174
DB 140 SSASTKGPVPEPLAPCSRSTSGTALGCLVKDYFPEPVTVSNMGSALTSGVHTFPAVLQ 199
QY 175 SSGLYSLSSVTVTPSSSLGTYTCYCNVDHKPSNTKVDKRVSK--YGPCCPAPBFL 231
DB 200 SSGLYSLSSVTVTPSSSLGTYTCYCNVDHKPSNTKVDKRVSKCDKTHTPCPAPBFL 259
QY 232 GGPVPEPLAPKPTLMISRTPEVTCVVDVSOEDPEVQFMWYDGVENHAKTKPREQ 291
DB 260 GGPVPEPLAPKPTLMISRTPEVTCVVDVSHEDPEVQFMWYDGVENHAKTKPREQ 319
QY 292 FNSTYRVSVTLTVLHODWLNGEKYCKVSNKGLPSSIEKTIKSKAKQPREQVYTLPPSQ 351
DB 320 YNSTYRVSVTLTVLHODWLNGEKYCKVSNKGLPSSIEKTIKSKAKQPREQVYTLPPSR 379
QY 352 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLRLLVDKS 411
DB 380 DELTGNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLRLLVDKS 439
QY 412 RMQGNVFCGVMEALHNHYTQKSLSLGLK 443
DB 440 RMQGNVFCGVMEALHNHYTQKSLSLGLK 471

RESULT 2
Q8TC63 PRELIMINARY; PRT: 473 AA.
ID Q8TC63
AC Q8TC63
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strauberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC025985; AAH25985.1;
DR InterPro; IPR000923; Bluec1.
DR InterPro; IPR007110; Ig_Like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00196; COPPER_BLUE; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 3.
KM Hypothetical protein.
SQ SEQUENCE 473 AA; 51986 MW; E29920B09BA369F5 CRC64;

Query Match 86.2%; Score 2032; DB 4; Length 473;
Best Local Similarity 86.1%; Pred. No. 86-161;
Matches 384; Conservative 24; Mismatches 34; Indels 4; Gaps 2;

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DB 208 LYSLSVTVTPSSSLGTYTCYCNVDHKPSNTKVDKRVSKYGPCCPAPBFLGSPVF 267
QY 238 LFPPKPTLMISRTPEVTCVVDVSOEDPEVQFMWYDGVENHAKTKPREQFNSTYR 297
DB 268 LFPPKPTLMISRTPEVTCVVDVSOEDPEVQFMWYDGVENHAKTKPREQFNSTYR 327
QY 298 VVSIVTLVHODWLNGEKYCKVSNKGLPSSIEKTIKSKAKQPREQVYTLPPSQEEMTKN 357
DB 328 VVSIVTLVHODWLNGEKYCKVSNKGLPSSIEKTIKSKAKQPREQVYTLPPSQEEMTKN 387
QY 358 QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLRLLVDKS 417
DB 388 QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLRLLVDKS 447
QY 418 VFSGVMEALHNHYTQKSLSLGLK 443
DB 448 VFSGVMEALHNHYTQKSLSLGLK 473

RESULT 3
Q8N4Y9 PRELIMINARY; PRT: 521 AA.
ID Q8N4Y9
AC Q8N4Y9
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells from Tonsils;
RA Strauberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC033178; AAH33178.1;
DR InterPro; IPR007110; Ig_Like.
DR InterPro; IPR003597; Ig_C1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_4.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 2.
KM Hypothetical protein.
SQ SEQUENCE 521 AA; 57156 MW; 2AC7D22E72DCAA2 CRC64;

Query Match 84.5%; Score 1990.5; DB 4; Length 521;
Best Local Similarity 76.5%; Pred. No. 2.6e-157;
Matches 384; Conservative 24; Mismatches 35; Indels 59; Gaps 3;

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OM protein - protein search, using sw model

Run on: December 31, 2003, 10:33:16 ; Search time 45.6667 Seconds

(without alignments)
1539.764 Million cell updates/sec

Title: US-09-917-410-4

Perfect score: 2357
Sequence: 1 EVOLVESGGGLVPGGSLRL.....MHEALHNHYTQKSLSLGLK 443

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

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23: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*
24: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2357	100.0	443	AAW13564	Humanised anti-L-6
2	2253.5	95.6	467	AA80617	Anti-human IL-4 hu
3	2139	90.8	447	AAW10232	TF8-569 CDR-grafted
4	2123.5	90.1	467	ABP71365	Anti-OPGL-1 antibo
5	2120.5	90.0	447	AAE33522	Human AQC2 heavy c
6	2120	89.9	470	ABG77158	Germline protein s
7	2114.5	89.7	447	AAE33523	Human AQC2 heavy c
8	2113.5	89.7	447	AAE33524	Human AQC2 heavy c
9	2113	89.6	474	AAO14065	Heavy chain protei

10	2113	89.6	474	24	ABU08017	Human monoclonal r
11	2111	89.6	449	21	AAE6810	A rat heavy chain
12	2109.5	89.5	449	23	AAO18400	Mature humanised m
13	2105	89.3	449	24	ABP58273	Humanised 3D6 anti
14	2105	89.3	468	24	ABP58275	Humanised 3D6 anti
15	2101	89.1	470	23	ABG77157	Amino acid sequenc
16	2098.5	89.0	444	24	AAE34676	BiMA/8 antibody h
17	2096.5	88.9	442	24	ABE80109	Heavy chain. Homo
18	2096.5	88.9	442	24	ABR39465	Humanised anti-Abe
19	2096.5	88.9	442	24	ABU08311	Humanised 266 anti
20	2096.5	88.9	461	22	AAU07745	Humanised monoclon
21	2096	88.9	468	13	AAE28808	pre-5A8 humanised
22	2093	88.8	470	23	AAU74298	Anti-human AILIM m
23	2093	88.8	470	23	AAU74300	Anti-human AILIM m
24	2090	88.7	451	22	AAU12715	Human recombinant
25	2090	88.7	451	24	ABU58807	Mucin 1 (MUC-1) b1
26	2089.5	88.7	473	23	ABG77162	Germline protein s
27	2089.5	88.7	477	22	AAU14288	Human novel protei
28	2087.5	88.6	463	21	AAV93707	The heavy chain of
29	2087.5	88.6	463	21	AAV93732	The heavy chain of
30	2086.5	88.5	442	24	ABR80113	Deglycosylated hea
31	2086.5	88.5	442	24	ABR39474	Humanised anti-Abe
32	2086.5	88.5	442	24	ABU08320	Humanised antibody
33	2083	88.4	464	21	AAV93703	The heavy chain of
34	2083	88.4	464	21	AAV93730	The heavy chain of
35	2083	88.4	464	21	ABG77161	Amino acid sequenc
36	2081.5	88.3	463	23	AAV93701	The heavy chain of
37	2081.5	88.3	463	21	AAV93727	The heavy chain of
38	2081	88.3	451	21	AAV93734	The heavy chain of
39	2080.5	88.3	450	24	ABP6294	4A5-3.1.1-B4 anti b
40	2078	88.2	464	18	AAW14941	3F4 Human IgG4 exp
41	2078	88.2	464	18	AAW14938	Murine anti-porcine
42	2078	88.2	582	22	AAE81987	Ganglioside GD3 sp
43	2076	88.1	466	13	AAE24812	Sequence encoded b
44	2075.5	88.1	463	21	AAV93728	The heavy chain of
45	2071	87.9	462	22	AAE72234	Humanised 323/A3 (

ALIGNMENTS

RESULT 1	
AAW13564	standard; Protein; 443 AA.
ID	AAW13564
XX	
AC	AAW13564;
XX	
DT	03-JUN-1997 (first entry)
XX	
DE	Humanised anti-L-selectin antibody Hudreg 55 heavy chain.
XX	
KW	L-selectin; humanised antibody; Hudreg 55; acute organ damage;
KW	organ failure; poly-trauma; haemorrhagic-traumatic shock.
XX	
OS	Chimeric Mus sp.;
OS	Chimeric Homo sapiens.
XX	
PN	W09706822-A1.
XX	
PD	27-FEB-1997.
XX	
PF	14-AUG-1996; 96MO-US13152.
XX	
PR	27-DEC-1995; 95US-0578953.
PR	17-AUG-1995; 95EP-0112895.
PR	19-SEP-1995; 95EP-0114696.
XX	
PA	(BOEF) BOEHRINGER MANNHEIM GMBH.
XX	(PROT-) PROTEIN DESIGN LABS INC.
XX	
PI	Co M, Haselbeck A, Martin U, Schumacher G;
DR	WPI; 1997-165036/15.

DR N-PSDB; AAT61281.
 XX Using anti-selectin antibody to prevent acute organ damage and
 PT multiple organ failure - during extracorporeal circulation or
 PT following polytrauma, e. g. haemorrhagic-traumatic shock
 XX
 PS Disclosure; Page 34-36; 52pp; English.
 XX
 CC Humanised anti-L-selectin antibody Hddreg 55 comprises 2 heavy
 CC chains each having the sequence given in AAW13564 and 2 light chains
 CC each having the sequence given in AAW13563. These are encoded by the
 CC cDNA clones given in AAT61281 and AAT61280. Hddreg 55 can be used to
 CC prevent multiple organ failure associated with polytrauma and for
 CC the prevention of acute organ damage associated with extracorporeal
 CC blood circulation. The antibody inhibits interaction between the
 CC carbohydrate-recognising domain of the selectin and the
 CC corresponding cell surface receptor.
 CC
 XX Sequence 443 AA:
 SQ
 Query Match 100.0%; Score 2357; DB 18; Length 443;
 Best Local Similarity 100.0%; Pred. No. 5,4e-137;
 Matches 443; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMSVAQAPKGLWEVASISTGSTYYP 60
 DB 1 EVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMSVAQAPKGLWEVASISTGSTYYP 60
 QY 61 DSVKRFITISRDNAKNTLYLQNSLRADDAVYVCARDYDGFYWGQGLTVTVSSASTK 120
 DB 61 DSVKRFITISRDNAKNTLYLQNSLRADDAVYVCARDYDGFYWGQGLTVTVSSASTK 120
 QY 121 GPSVPEPLAPCSRSTSESTALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYS 180
 DB 121 GPSVPEPLAPCSRSTSESTALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYS 180
 QY 181 LSSVTVTPSSSLGTITTCNVDHKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSVFLFP 240
 DB 181 LSSVTVTPSSSLGTITTCNVDHKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSVFLFP 240
 QY 241 PRPKDTLMISRTPEVTCVVDVSOEDPEVQFMWYVDGVEVHNAKTRPREEQFNSTYRVAS 300
 DB 241 PRPKDTLMISRTPEVTCVVDVSOEDPEVQFMWYVDGVEVHNAKTRPREEQFNSTYRVAS 300
 QY 301 VITVLHODMLNGKEYCKVSNKGLPSSIEKITSKAKGQPREPQVYTLPPSOEEMTKNOVS 360
 DB 301 VITVLHODMLNGKEYCKVSNKGLPSSIEKITSKAKGQPREPQVYTLPPSOEEMTKNOVS 360
 QY 361 LTCLVKGFPYPSDIAVWESNGQPENNYKTPPVLDSDGSFFLYSRLTVDKSRWQEGNVS 420
 DB 361 LTCLVKGFPYPSDIAVWESNGQPENNYKTPPVLDSDGSFFLYSRLTVDKSRWQEGNVS 420
 QY 421 CSVMHEALHNHYTQKSLSLSTGK 443
 DB 421 CSVMHEALHNHYTQKSLSLSTGK 443

RESULT 2
 AAR80617
 ID AAR80617 standard; Protein; 467 AA.
 XX
 AC AAR80617;
 XX
 XX
 DT 19-APR-1996 (first entry)
 XX
 XX Anti-human IL-4 humanised MAb h25D2-9 mature heavy chain.
 DE Anti-human interleukin-4; IL-4; humanised; purification;
 XX treatment; IL-4 diseases; immunoassay; heavy chain; h25D2-9;
 KW antibody.
 XX
 XX Homo sapiens.
 OS
 XX

EH Key Location/Qualifiers
 FT Peptide 1..19
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 XX
 XX W09524481-A2.
 XX
 XX 14-SEP-1995.
 PD
 XX
 XX 08-MAR-1995; 95WO-US02400.
 PE
 XX 10-MAR-1994; 94US-0208886.
 PR
 XX (SCHE) SCHERING CORP.
 PA
 XX
 PI Dale B, Miller K, Murgolo N, Tindall S;
 XX
 XX WPI; 1995-328272/42.
 DR
 XX
 XX Humanised monoclonal antibody against human interleukin (IL)-4 -
 PT has increased binding affinity and expression, and hence greater
 PT therapeutic value in the treatment of IL-4 related diseases
 XX
 XX Claim 3; Pages 109-110; 116pp; English.
 PS
 XX
 XX AAR80617 is the anti-human IL-4 humanised monoclonal antibody (MAb)
 CC h25D2-9, mature heavy chain. It can be used for the prepn.,
 CC purificn. and immunoassay of the humanised Abs. Pharmaceutical
 CC compns. and anti-idiotypic Abs (against the MAb) can also be
 CC prepd. for the treatment of IL-4 related diseases by respectively
 CC suppressing, or imitating the binding activity of IL-4. The
 CC humanised MAb is derived from the rodent. MAb 25D2.
 CC
 XX
 SQ Sequence 467 AA:
 Query Match 95.6%; Score 2253.5; DB 16; Length 467;
 Best Local Similarity 95.3%; Pred. No. 1.3e-130;
 Matches 427; Conservative 11; Mismatches 5; Indels 5; Gaps 3;

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 DB 20 EVQLVESGGGLVQPGGSLRLSCAASGFTSTYMTWVROAPKGLWEVASISIGDNTY 79
 QY 60 PDSVKGFTISRDNAKNTLYLQNSLRADDAVYVCARD--YDG-YFDYWGQGLTVTVS 115
 DB 80 PDSVKGFTISRDNAKNTLYLQNSLRADDAVYVCARDYVYFSGHYFDYWGQGLTVTVS 139
 QY 116 SASIKGSPVPEPLAPCSRSTSESTALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 175
 DB 140 SASIKGSPVPEPLAPCSRSTSESTALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 199
 QY 176 SGLYSLSVTVTPSSSLGTITTCNVDHKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPS 235
 DB 200 SGLYSLSVTVTPSSSLGTITTCNVDHKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPS 259
 QY 236 VFLPPEPKDTLMISRTPEVTCVVDVSOEDPEVQFMWYVDGVEVHNAKTRPREEQFNST 295
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 QY 296 YRVVSVLTVLHODMLNGKEYCKVSNKGLPSSIEKITSKAKGQPREPQVYTLPPSOEEMT 355
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 QY 356 KNQVSLTCLVKGFPYPSDIAVWESNGQPENNYKTPPVLDSDGSFFLYSRLTVDKSRWQ 415
 DB 380 KNQVSLTCLVKGFPYPSDIAVWESNGQPENNYKTPPVLDSDGSFFLYSRLTVDKSRWQ 439
 QY 416 GNVSFCSVMHEALHNHYTQKSLSLSTGK 443
 DB 440 GNVSFCSVMHEALHNHYTQKSLSLSTGK 467

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 31, 2003, 10:32:16 ; Search time 34.3333 Seconds

(without alignments)
2588.856 Million cell updates/sec

Title: US-09-917-410-4

Perfect score: 2357
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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 733937 seqs, 200641211 residues

Total number of hits satisfying chosen parameters: 733937

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	2113	89.6	474	12	US-10-225-108A-3
4	2112	89.6	474	12	US-09-848-832-3
5	2112.5	89.6	445	12	US-10-220-231A-79
6	2111	89.6	449	10	US-09-736-371B-21
7	2106.5	89.4	448	9	US-09-917-410-6
8	2098.5	89.0	444	15	US-10-150-475A-6
9	2093	88.8	470	10	US-09-859-053-32
10	2093	88.8	470	10	US-09-859-053-36
11	2090	88.7	451	10	US-09-822-698A-26
12	2089.5	88.6	477	12	US-10-291-265-395
13	2087.5	88.6	463	15	US-10-153-382-13
14	2083	88.4	464	15	US-10-153-382-9
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ALIGNMENTS

RESULT 1

US-09-917-410-4

; Sequence 4, Application US/09917410

; Patent No. US20020098183A1

GENERAL INFORMATION:

APPLICANT: MARTIN, Ulrich; HASELBECK, Anton; SCHUMACHER, Guenther;

CO, Man S.

TITLE OF INVENTION: ANTI-L-SELECTIN ANTIBODIES FOR PREVENTION OF MULTIPLE ORGAN FAILURE AFTER POLYTRAUMA AND FOR PREVENTION OF ACUTE ORGAN DAMAGE AFTER EXTRACORPOREAL BLOOD CIRCULATION

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Felte & Lynch

STREET: 805 Third Avenue

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10022

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Computer Disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII, WordPerfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/917,410

FILING DATE: 26-Jul-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/578,953

FILING DATE: <Unknown>

APPLICATION NUMBER: EP 95 114 969.9

FILING DATE: 19-Sep-95

ATTORNEY/AGENT INFORMATION:

NAME: Hanson, Nc. US20020098183A1man D.

REGISTRATION NUMBER: 30,946

REFERENCE/DOCKET NUMBER: BOER 1059-PFF/NDH/SLH

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 443
TYPE: amino acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-917-410-4

Query Match 100.0%; Score 2357; DB 9; Length 443;
Best Local Similarity 100.0%; Pred. No. 4,9e-157;
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DB 1 EVOLVESGGGLVQPGGSLRLSCAASGFTSTYAMSVMVRQAPGKLEWVASISIGSGSIYYP 60
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DB 121 GPSVFPPLAPCSRSTSESTALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYS 180
QY 181 LSSVTVVSSSLGTITTCNVNDHKPSNTKVDKRVESKYGPPCPCPAPPEFLGSPVFLFP 240
DB 181 LSSVTVVSSSLGTITTCNVNDHKPSNTKVDKRVESKYGPPCPCPAPPEFLGSPVFLFP 240
QY 241 PAKKDTLMISRPEVTCVVDVDSQEDPEVQFMVYDGVENVNAKTKPREEOFNSTYRVS 300
DB 241 PAKKDTLMISRPEVTCVVDVDSQEDPEVQFMVYDGVENVNAKTKPREEOFNSTYRVS 300
QY 301 VLTVLHQMVLNGKEYKCVSNKGLPSSIEKTISSAKGQPREPOVYTLPPSQEEMTKNOVS 360
DB 301 VLTVLHQMVLNGKEYKCVSNKGLPSSIEKTISSAKGQPREPOVYTLPPSQEEMTKNOVS 360
QY 361 LTCLVKGFPYPSDIAVWESNGQPENNYKTTPPVLDSDGSFLYSRLTYDKSRWQDGN 420
DB 361 LTCLVKGFPYPSDIAVWESNGQPENNYKTTPPVLDSDGSFLYSRLTYDKSRWQDGN 420
QY 421 CSVMHEALHNHYTQKSLSLGLK 443
DB 421 CSVMHEALHNHYTQKSLSLGLK 443

RESULT 2

US-10-401-344-2
Sequence 2, Application US/10401344
Publication No. US20030194404A1
GENERAL INFORMATION:
APPLICANT: Schering Corporation and Abgenix, Inc.
APPLICANT: Greenfeder, Scott
APPLICANT: Corvaelan, Jose
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO INTERLEUKIN-5 AND METHODS AND COM
TITLE OF INVENTION: COMPRISING SAME
FILE REFERENCE: L101564W1
CURRENT APPLICATION NUMBER: US/10/401,344
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 465
TYPE: PRM
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SIGNAL
LOCATION: (1)..(19)
OTHER INFORMATION:
FEATURE:

NAME/KEY: Variable Region
LOCATION: (20)..(138)
OTHER INFORMATION:
FEATURE:
NAME/KEY: CH1 Region
LOCATION: (139)..(236)
OTHER INFORMATION:
FEATURE:
NAME/KEY: Hinge Region
LOCATION: (237)..(248)
OTHER INFORMATION:
FEATURE:
NAME/KEY: CH2 Region
LOCATION: (249)..(358)
OTHER INFORMATION:
FEATURE:
NAME/KEY: CH3 Region
LOCATION: (359)..(465)
OTHER INFORMATION:
US-10-401-344-2

Query Match 96.2%; Score 2266.5; DB 12; Length 465;
Best Local Similarity 96.4%; Pred. No. 1.1e-150;
Matches 430; Conservative 9; Mismatches 4; Indels 3; Gaps 3;

QY 1 EVOLVESGGGLVQPGGSLRLSCAASGFTSTYAMSVMVRQAPGKLEWVASIS-TGSGSIY 59
DB 20 EVOLVESGGGLVQPGGSLRLSCAASGFTSTYAMSVMVRQAPGKLEWVASIS-TGSGSIY 79
QY 60 PDSYKGRFTISRDNKNTLYIQMNSLRADDAVYVCARD-YD-GYFDYWGQGLTVTVSSA 117
DB 80 ADSYKGRFTISRDNKNTLYIQMNSLRADDAVYVCARDYNAKRYNNVYLNHMGQGLTVTVSSA 139
QY 118 STKGPSVFPPLAPCSRSTSESTALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG 177
DB 140 STKGPSVFPPLAPCSRSTSESTALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG 199
QY 178 LYSLSVTVVSSSLGTITTCNVNDHKPSNTKVDKRVESKYGPPCPCPAPPEFLGSPVFL 237
DB 200 LYSLSVTVVSSSLGTITTCNVNDHKPSNTKVDKRVESKYGPPCPCPAPPEFLGSPVFL 259
QY 238 LFPKPKDTLMISRPEVTCVVDVDSQEDPEVQFMVYDGVENVNAKTKPREEOFNSTYR 297
DB 260 LFPKPKDTLMISRPEVTCVVDVDSQEDPEVQFMVYDGVENVNAKTKPREEOFNSTYR 319
QY 298 VVSVLTVLHQMVLNGKEYKCVSNKGLPSSIEKTISSAKGQPREPOVYTLPPSQEEMTKN 357
DB 320 VVSVLTVLHQMVLNGKEYKCVSNKGLPSSIEKTISSAKGQPREPOVYTLPPSQEEMTKN 379
QY 358 QVSLTCLVKGFPYPSDIAVWESNGQPENNYKTTPPVLDSDGSFLYSRLTYDKSRWQDGN 417
DB 380 QVSLTCLVKGFPYPSDIAVWESNGQPENNYKTTPPVLDSDGSFLYSRLTYDKSRWQDGN 439
QY 418 VFCSCVMHEALHNHYTQKSLSLGLK 443
DB 440 VFCSCVMHEALHNHYTQKSLSLGLK 465

RESULT 3

US-10-225-108A-3
Sequence 3, Application US/10225108A
Publication No. US20030157112A1
GENERAL INFORMATION:
APPLICANT: HOOPER, Craig
APPLICANT: DIETRISCHOLD, Bernhard
TITLE OF INVENTION: Recombinant Antibodies, and Compositions
TITLE OF INVENTION: and Methods for Making Them
FILE REFERENCE: 8321-110
CURRENT APPLICATION NUMBER: US/10/225,108A
CURRENT FILING DATE: 2003-04-10
PRIOR APPLICATION NUMBER: US 09/848,832
PRIOR FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: US 60/204,518

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 31, 2003, 10:29:11 ; Search time 8.44244 Seconds

(without alignments)
2506.043 Million cell updates/sec

Title: US-09-917-410-5

Perfect score: 1142

Sequence: 1 DIQMTQSPSTLSASVGRVT.....EVTHQGLSSPVTKSFNRGEC 220

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	945.5	82.8	215	2	JE0242	Ig kappa chain NIG
2	917.5	80.3	215	2	JE0244	Ig kappa chain NIG
3	908	79.5	216	2	JE0241	Ig kappa chain NIG
4	894.5	78.3	215	2	A23746	Ig kappa chain V-I
5	891.5	78.1	215	2	JE0243	Ig kappa chain NIG
6	824	72.2	240	2	S06084	Ig kappa chain NIG
7	813	71.2	214	2	S68212	Ig kappa chain pre
8	790	69.2	220	2	A31790	Ig kappa chain (Ma
9	717	62.8	230	2	S33161	Ig kappa chain V r
10	714.5	62.6	225	2	S37484	Ig kappa chain - m
11	705.5	61.8	219	2	S38655	Ig kappa chain - s
12	701.5	61.4	217	2	S42772	Ig kappa chain - m
13	699	61.2	234	2	S01320	Ig kappa chain - m
14	693.5	60.7	219	2	PC4203	Ig kappa chain pre
15	693.5	60.7	219	2	SS2028	Ig kappa chain (mo
16	691.5	60.6	219	2	S16112	Ig kappa chain - m
17	685	60.0	234	2	S14237	Ig kappa chain V r
18	681	59.6	218	2	S68241	Ig kappa chain pre
19	679	59.5	218	2	JC5810	Ig kappa chain V r
20	665.5	58.3	225	2	JL0029	Ig kappa chain V r
21	657.5	57.6	235	2	S25058	Ig kappa chain pre
22	649	56.8	210	2	A56169	Ig kappa chain - m
23	605	53.0	135	2	SS2059	Ig kappa chain V r
24	601	52.6	178	2	PT0219	Ig kappa chain V-C
25	554.5	48.0	106	1	A20969	Ig kappa chain pre
26	548	48.0	106	1	K3HU	Ig kappa chain V r
27	539.5	47.2	197	2	A49633	Ig kappa chain V r
28	532.5	46.6	197	2	S29593	Ig kappa chain (Ma
29	513	44.9	99	2	A37927	Ig kappa chain C r

30	507	44.4	99	2	S26653	Ig kappa chain C r
31	487	42.6	113	2	JC2270	PL7-6 antibody lig
32	483	42.3	109	2	S26336	Ig light chain V r
33	482	42.2	145	2	PL0014	Ig kappa chain pre
34	475	41.6	233	2	S29577	Ig light chain - r
35	474	41.5	141	2	A49134	Ig kappa chain V-I
36	472.5	41.4	145	2	S20631	Ig kappa chain - h
37	471	41.2	120	2	S51147	Ig kappa chain V-I
38	470	41.2	114	1	K4HUN	Ig kappa chain V-I
39	470	41.2	144	2	PL0106	Ig kappa chain V-I
40	469	41.1	127	2	S40367	Ig kappa chain V-I
41	468	41.0	113	2	S34002	Ig kappa chain V-I
42	462	40.5	114	2	S44119	Ig kappa chain V-I
43	461	40.4	108	2	B49047	Ig kappa chain V-I
44	460	40.3	134	2	S49531	Ig kappa chain V r
45	459	40.2	134	1	K4H17	Ig kappa chain V r

ALIGNMENTS

RESULT 1

JE0242
Ig kappa chain NIG2 precursor - human
C/Species: Homo sapiens (man)
C/Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C/Accession: JE0242
R/Alim, M.A.; Yamaki, S.; Hossein, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda, submitted to JIPID, November 1998
A/Description: Structure relationship of kappa type light chains with AL amyloidosis: Mu
A/Reference number: JE0241
A/Accession: JE0242
A/Molecule type: protein
A/Residues: 1-215 <ALI>
C/Superfamily: immunoglobulin V region; immunoglobulin homology
F16-91/Domain: immunoglobulin homology <IMV>

Query Match 82.8%; Score 945.5; DB 2; Length 215;
Best Local Similarity 81.8%; Pred. No. 2.7e-59;
Matches 180; Conservative 17; Mismatches 18; Indels 5; Gaps 1;

QY	1	DIQMTQSPSTLSASVGRVTITTKSSQSLNSNKNYLAAYQKQKAPKLIVFASTR	60
DB	1	EIVLTQSPGTLISLSPERATLSCRASQSVN-----NYLAAYQKQKQAPSLIIVDASR	55
QY	61	ESGVPRFGSSGSGTDFTLITSSLOPEDPATYFCHQHYSTPLTFGGCTKVEKRYVAAPS	120
DB	56	ATGIPRFSSGSGGTFILITSLGLEPEDFAVYCCQYDRPMTFGGCTKVEIKRYVAAPS	115
QY	121	VFIFFPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS	180
DB	116	VFIFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS	175
QY	181	LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	220
DB	176	LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	215

RESULT 2

JE0244
Ig kappa chain NIG2 precursor - human
C/Species: Homo sapiens (man)
C/Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C/Accession: JE0244
R/Alim, M.A.; Hara, Y.; Hossein, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.; submitted to JIPID, November 1998
A/Description: A new subgroup of kappa type light chains (VKV) identified in cases of AL am
A/Reference number: JE0243
A/Accession: JE0244
A/Molecule type: protein
A/Residues: 1-215 <ALI>
C/Superfamily: immunoglobulin V region; immunoglobulin homology
F16-90/Domain: immunoglobulin homology <IMV>

```

Query Match      80.3%; Score 917.5; DB 2; Length 215;
Best Local Similarity 81.5%; Pred. No.2,4e-57;
Matches 181; Conservative 18; Mismatches 14; Indels 9; Gaps 4;

QY 1 DIQMTPSPSTLASVGDRTVITTKSSQSGLNSNNQKNTLAMYQKFGKAPKLLVYFASR 60
Db 1 EVLTQSPATLSVSPGRATLSCRASQSV--HSN----LAWYQKFGQAPRLLIYASR 54
QY 61 ESGVPPDRFICSGSGTDFLTLLTSLQPEDFATFYCHQHSY--PLTFGCGKTKVEKRTVA 118
Db 55 ATGIPARFSSGSGGTDFLTLLTSLQSEDFALYLC-QQNTWPLTITGGTKEIKRTVA 113
QY 119 PSYFIFPPSDQKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDT 178
Db 114 PSYFIFPPSDQKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDT 173
QY 179 YSLSTLTLSKADYEKHKVYACEVTHQGLSSPTTKSFNRGEC 220
Db 174 YSLSTLTLSKADYEKHKVYACEVTHQGLSSPTTKSFNRGEC 215

RESULT 3
JE0241
IG kappa chain AmJ7 precursor - human
C:Species: Homo sapiens (man)
C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C:Accession: JE0241
R:Altun, M.A.; Yamaki, S.; Hoesain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda, T.
A:Description: Structure relationship of kappa type light chains with AL amyloidosis. Mol
A:Reference number: JE0241
A:Accession: JE0241
A:Molecule type: protein
A:Residues: 1-216 <ALI>
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
F:16-92/Domain: immunoglobulin homology <IMM>

Query Match      79.5%; Score 908; DB 2; Length 216;
Best Local Similarity 80.9%; Pred. No.1,1e-56;
Matches 178; Conservative 17; Mismatches 21; Indels 4; Gaps 3;

QY 1 DIQMTPSPSTLASVGDRTVITTKSSQSGLNSNNQKNTLAMYQKFGKAPKLLVYFASR 60
Db 1 DIVLTQSPDFLAVSLGERATINCKSSQSVL--YNSKNFLAWYQKPGQ-PKLLTW-ANVR 56
QY 61 ESGVPPDRFICSGSGNDFTLLTSLQPEDFATFYCHQHSY--PLTFGCGTKEVEKRTVA 120
Db 57 ESGVPPDRFICSGSGNDFTLLTSLQPEDFATFYCHQHSY--PLTFGCGTKEVEKRTVA 116
QY 121 VFIFPPSDQKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDT 180
Db 117 VFIFPPSDQKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDT 176
QY 181 LSSTLTLSKADYEKHKVYACEVTHQGLSSPTTKSFNRGEC 220
Db 177 LSSTLTLSKADYEKHKVYACEVTHQGLSSPTTKSFNRGEC 216

RESULT 4
A23746
IG kappa chain V-III (KAU cold agglutinin) - human
C:Species: Homo sapiens (man)
C:Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 21-Jan-2000
C:Accession: A23746
R:Leon, J.; Ghico, J.; Goni, F.; Frangione, B.
J. Biol. Chem. 265, 2836-2842, 1991
A:Title: The primary structure of the Fab fragment of protein KAU, a monoclonal immunog
A:Reference number: A23746; PMID:1993660
A:Accession: A23746
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-215 <LBO>

```

C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:16-91/Domain: immunoglobulin homology <IMM>

Query Match 78.3%; Score 894.5; DB 2; Length 215;
Best Local Similarity 80.4%; Pred. No. 9.6e-56;
Matches 176; Conservative 19; Mismatches 19; Indels 5; Gaps 1;

QY 1 DIQMTGSPSTLASVGDRTVITTKSSQSGLNSNQKRYLAMYOQKPGKAPKLLVYFPASTR 60
Db 1 EIVLTGSPATLSPGGRATLISGASQSV-----SSNYLMYQKPGQAPRLRLTYDASSR 55
QY 61 ESGVPDFEFGSGSGTDFLTITSLQPEDFATYFCHQHYSTPLTFGGTRKVEKRTVAAPS 120
Db 56 ATGIPDRFSGSGSGTDFLTITSLRLEPDEFATYFQYQSSPLTGGGTRKVEKRTVAAPS 115
QY 121 VFIFPPSDQKSGSTASVCLNNFYPREAKYQKVDNALQSGNSQESYTFEODSKDSTYS 180
Db 116 VFIFPPSDQKSGSTASVCLNNFYPREAKYQKVDNALQSGNSQESYTFEODSKDSTYS 175
QY 181 LSTTITLTKADYEKHKVYACEVTHQGLSPPTKSFNNGE 219
Db 176 LSTTITLTKADYEKHKVYAGEVTHQGLSPPTKSFNNGE 214

RESULT 5
JB0243
Ig kappa chain NIG93 precursor - human
C:Species: Homo sapiens (man)
C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C:Accession: JB0243
R:Alim, M.A.; Hara, Y.; Hosasin, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.;
Submitted to JRPID, November 1998
A:Description: A new subgroup of k type light chains (VKV) identified in cases of AL am
A:Reference number: JB0243
A:Accession: JB0243
A:Molecule type: protein
A:Residues: 1-215 <ALT>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 78.1%; Score 891.5; DB 2; Length 215;
Best Local Similarity 79.2%; Pred. No. 1.6e-55;
Matches 175; Conservative 18; Mismatches 21; Indels 7; Gaps 2;

QY 1 DIQMTGSPSTLASVGDRTVITTKSSQSGLNSNQKRYLAMYOQKPGKAPKLLVYFPASTR 60
Db 1 EIVMTGSPATLSPGGRATLISCRASQSVATN-----VVMYQKPGQAPRLRLTYDASSR 54
QY 61 ESGVPDRFEGSGSGTDFLTITSLQPEDFATYFCHQHYSTPLTFGGTRKVEK-RTVAAP 119
Db 55 ATGVPARFSGSGSGTDFLTITSLQSEDFATYFCHNNAMPPTFGGTRKVEKRTVAAP 114
QY 120 VFIFPPSDQKSGSTASVCLNNFYPREAKYQKVDNALQSGNSQESYTFEODSKDSTY 179
Db 115 VFIFPPSDQKSGSTASVCLNNFYPREAKYQKVDNALQSGNSQESYTFEODSKDSTY 174
QY 180 SLSTTITLTKADYEKHKVYACEVTHQGLSPPTKSFNNGEC 220
Db 175 SLSTTITLTKADYEKHKVYACEVTHQGLSPPTKSFNNGEC 215

RESULT 6
S06084
Ig kappa chain precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 21-Jan-2000
C:Accession: S06084
R:Crowe, J.S.; Smith, M.A.; Cooper, H.J.
Nucleic Acids Res 17, 7992, 1989
A:Title: Nucleotide sequence of γ 1-Ag 1.2.3, rat myeloma immunoglobulin kappa chain CD
A:Reference number: S06084; MUID:90016888; EMD:2508067
A:Accession: S06084

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OM protein - protein search, using sw model

Run on: December 31, 2003, 10:29:10 ; Search time 5.29722 Seconds

(without alignments)
1953.078 Million cell updates/sec

Title: US-09-917-410-5

Perfect score: 1142

Sequence: 1 DIQMTQSPSTLSASVGRVT.....EYTHQGLSSPVTKSHNGEC 220

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwisProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	548	48.0	106 1 KAC_HUMAN	P01834 homo sapien
2	469	41.1	114 1 KV4A_HUMAN	P01625 homo sapien
3	462	40.5	134 1 KV4C_HUMAN	P06314 homo sapien
4	445	39.0	108 1 KV1B_HUMAN	P01600 homo sapien
5	440.5	38.6	133 1 KV1H_HUMAN	P06313 homo sapien
6	435	38.1	108 1 KV1F_HUMAN	P01598 homo sapien
7	434	38.0	129 1 KV1V_HUMAN	P04431 homo sapien
8	433	37.9	108 1 KV1W_HUMAN	P04430 homo sapien
9	429	37.6	108 1 KV1M_HUMAN	P01605 homo sapien
10	426	37.3	108 1 KV1S_HUMAN	P01611 homo sapien
11	421	36.9	108 1 KV1K_HUMAN	P01603 homo sapien
12	419	36.7	108 1 KV1C_HUMAN	P01603 homo sapien
13	419	36.7	108 1 KV1R_HUMAN	P01610 homo sapien
14	417	36.5	108 1 KV1E_HUMAN	P01597 homo sapien
15	417	36.5	121 1 KV4E_HUMAN	P06312 homo sapien
16	416.5	36.5	107 1 KV1D_HUMAN	P01596 homo sapien
17	415	36.3	108 1 KV1N_HUMAN	P01606 homo sapien
18	415	36.3	109 1 KV4D_HUMAN	P03553 homo sapien
19	414	36.3	108 1 KV1G_HUMAN	P01599 homo sapien
20	414	36.3	108 1 KV1L_HUMAN	P01604 homo sapien
21	413	36.2	108 1 KV1B_HUMAN	P01594 homo sapien
22	412	36.1	108 1 KV1O_HUMAN	P01607 homo sapien
23	412	36.1	108 1 KV1P_HUMAN	P08032 homo sapien
24	406	35.6	108 1 KV1D_HUMAN	P01608 homo sapien
25	405.5	35.5	109 1 KV3D_HUMAN	P01622 homo sapien
26	405	35.5	109 1 KV3B_HUMAN	P01609 homo sapien
27	402.5	35.2	108 1 KV1Q_HUMAN	P01620 homo sapien
28	401.5	34.9	108 1 KV1A_HUMAN	P01593 homo sapien
29	399	34.9	108 1 KV3L_HUMAN	P01593 homo sapien
30	398.5	34.6	109 1 KV3M_HUMAN	P01816 homo sapien
31	395.5	34.3	109 1 KV1T_HUMAN	P01612 homo sapien
32	392	34.3	129 1 KV1X_HUMAN	P04432 homo sapien
33	390	34.2	112 1 KV1U_HUMAN	P01613 homo sapien

ALIGNMENTS

34	390	34.2	149	1	KV5A_MOUSE	P01633 mus musculu
35	387.5	33.9	109	1	KV3E_HUMAN	P04206 homo sapien
36	386.5	33.8	109	1	KV3E_HUMAN	P01623 homo sapien
37	386	33.8	117	1	KV1U_HUMAN	P01602 homo sapien
38	383.5	33.6	109	1	KV3F_HUMAN	P01624 homo sapien
39	382	33.5	108	1	KV5D_MOUSE	P01636 mus musculu
40	379.5	33.2	108	1	KV3A_HUMAN	P01619 homo sapien
41	374	32.7	114	1	KV1A_MOUSE	P01632 mus musculu
42	372	32.6	108	1	KV5M_MOUSE	P01646 mus musculu
43	369	32.3	108	1	KV5J_MOUSE	P01643 mus musculu
44	369	32.3	117	1	KV1I_HUMAN	P01601 homo sapien
45	368.5	32.3	129	1	KV3H_HUMAN	P04207 homo sapien

RESULT 1
KAC_HUMAN STANDARD; PRT; 106 AA.
ID AC P01834;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE 1g kappa chain C region.
GN IGKC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE (MYELOMA PROTEIN EU).
RX MEDLINE=71064023; PubMed=5469770;
RA Gettlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. VI. Amino
RL acid sequence of the light chain.";
RL Biochemistry 9:3155-3161(1970).
RN [2]
RP DISULFIDE BONDS.
RX MEDLINE=71064027; PubMed=4923144;
RA Gall W.E., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. X.
RL Intrachain disulfide bonds.";
RL Biochemistry 9:3188-3196(1970).
RN [3]
RP SEQUENCE (BENCE-JONES PROTEIN TI).
RX MEDLINE=72186439; PubMed=5027703;
RA Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
RT immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein
RT TI). IV. The complete amino acid sequence and its significance for
RL the mechanism of antibody production.";
RL Hoppe-Seyler's Z. Physiol. Chem. 353:189-208(1972).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=81042304; PubMed=6775818;
RA Hietzer P.A., Max E.E., Seidman J.G., Matzel J.V., Jr., Leder P.;
RT "Cloned human and mouse kappa immunoglobulin constant and J region
RL genes conserve homology in functional segments.";
RL Cell 22:197-207(1980).
RN [5]
RP SEQUENCE (BENCE-JONES PROTEIN ROY).
RA Hilschmann N., Barnikol H.U., Hess M., Langer B., Ponstingl H.,
RA Steimeretz-Kayne M., Suter L., Watanabe S.;
RL (in) Franek F., Shugar D. (eds.),
RL Gamma globulins: structure and function, pp.57-74, Academic Press,
RN New York (1969).
RN [6]
RP SEQUENCE (BENCE-JONES PROTEIN CUM).
RX MEDLINE=68242259; PubMed=5586923;
RA Hilschmann N.;
RT "The complete amino acid sequence of Bence Jones protein Cum (kappa-
RT type).";

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 31, 2003, 10:33:16 ; Search time 22.6787 Seconds

(without alignments)
1539.764 Million cell updates/sec

Title: US-09-917-410-5

Perfect score: 1142 1 DIOMTOSPTLSASVGDRTV.....EVTHQGLSEPTKSKFNRGEC 220

Sequence: 1 DIOMTOSPTLSASVGDRTV.....EVTHQGLSEPTKSKFNRGEC 220

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing:

Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	1057	92.6	242	AAU97949
2	1057	92.6	242	AAU80039
3	1057	92.6	242	AAU80338
4	1011	88.5	240	AAU50161
5	1009	88.4	214	AAU93735
6	1009	88.4	240	AAU00815
7	1007	88.2	240	AAE87927
8	1007	88.2	240	AAE82836
9	1000.5	87.6	242	AAU29436

10	1000.5	87.6	242	21	AAE30320	Humanised anti-IL-
11	1000.5	87.6	242	21	AAU77763	Humanised anti-IL-
12	1000.5	87.6	242	24	AAU59510	Humanised Mouse an
13	1000.5	87.6	242	24	AAU13797	Humanised mouse an
14	1000	87.6	220	18	AAU07528	Anti-HGF receptor
15	999	87.5	244	21	AAU96305	Human IGFAM-17 imm
16	998.5	87.4	242	19	AAU69302	Humanised anti-IL-
17	998.5	87.4	242	20	AAU29453	Humanised anti-IL-
18	998.5	87.4	242	21	AAU30313	Humanised anti-IL-
19	998.5	87.4	242	21	AAU77756	Humanised anti-IL-
20	998.5	87.4	242	24	AAU59503	Humanised Mouse an
21	998.5	87.4	242	24	AAU13790	Humanised mouse an
22	997.5	87.3	219	20	AAU29459	Recombinant immuno
23	997.5	87.3	219	21	AAU30323	Humanised anti-IL-
24	997.5	87.3	219	21	AAU77767	Humanised anti-IL-
25	997.5	87.3	219	24	AAU59513	Humanised Mouse an
26	997.5	87.3	219	24	AAU13800	Humanised mouse an
27	997.5	87.3	237	21	AAU966298	Human IGFAM-10 imm
28	997.5	87.3	242	19	AAU69313	Anti-IL-8 humanise
29	997.5	87.3	242	19	AAU69301	Humanised anti-IL-
30	997.5	87.3	242	20	AAU29435	Humanised anti-IL-
31	997.5	87.3	242	21	AAU30317	6G4-2-5V1IN35A 11g
32	997.5	87.3	242	21	AAU77760	Humanised anti-IL-
33	997.5	87.3	242	24	AAU59507	Humanised Mouse an
34	997.5	87.3	242	24	AAU13794	Humanised mouse an
35	996	87.2	240	24	AAU38594	Hepatitis C virus
36	994.5	87.1	241	22	AAU82812	Human immune respo
37	994	87.0	260	23	AAU41164	Human ovarian anti
38	993.5	87.0	237	21	AAU96289	Human IGFAM-1 immu
39	992	86.9	363	22	AAU14228	Human novel protei
40	991	86.8	214	18	AAU34504	Light chain of hum
41	991	86.8	214	18	AAU34506	Human antibody huH
42	991	86.8	214	20	AAU08754	Humanized anti-CD1
43	991	86.8	214	20	AAU95615	Recombinant human
44	991	86.8	214	20	AAU30632	rhumAb CD18 light
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ALIGNMENTS

RESULT 1
AAU97949 standard; Protein; 242 AA.
XX
AC AAU97949;
XX
DT 19-AUG-2002 (first entry)
XX
DE HMFGL FabI caspase 3 fusion construct protein #2.
XX
KW Pro-caspase-3; apoptosis; cell targeting; HMFGL FabI fusion protein;
KM cancer; cytotoxic; caspase.
XX
OS Unidentified.
XX
PN GB2360772-A.
XX
PD 03-OCT-2001.
XX
PF 28-MAR-2001; 2001GB-0007725.
XX
PR 28-MAR-2000; 2000GB-0007343.
XX
PA (ANTI-) ANTISOMA RES LTD.
XX
PI Epenetos AA;
XX
DR WPI; 2001-640889/74.
XX
DR N-PSDB; ABRX5864.
XX
PT New compounds comprising a mediator portion capable of recognising a
target cell-specific molecule, and a cytotoxic portion consisting of

PT caspase, useful for treating a disease associated with the dysfunction
PT of cells, e.g. cancer -

XX Examples; Fig 3; 85pp; English.

XX This invention relates to novel compounds comprising a target cell-
CC specific portion or a mediator portion capable of recognising a target
CC cell-specific molecule, and a cytotoxic portion. The compounds are
CC characterised in that the cytotoxic second portion is a constitutively
CC active caspase or has substantially the same apoptosis-inducing activity
CC as the caspases. The compounds of the invention may have cytostatic
CC activity. The compounds of the invention and compositions comprising
CC these compounds are useful in medicine, particularly useful in the
CC preparation of a medicament for treating a disease associated with the
CC dysfunction of a population of cells, such as cancer in humans. The
CC present sequence represents the HMFG1/Fab1 caspase 3 fusion protein
CC of the invention.

XX Sequence 242 AA;

Query Match 92.6%; Score 1057; DB 22; Length 242;
Best Local Similarity 92.7%; Pred. No. 1.4e-57;
Matches 204; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

QY 1 DIQMTQSPSTLSASVGDRTVITCKSSQSLNNSNQNYLAWYQKPKAKPLLYFPASTR 60
DB 23 DIQMTQSPSTLSASVGDRTVITCKSSQSLNNSNQNYLAWYQKPKAKPLLYFMASTR 82
QY 61 ESGVDRFRITGSGSGTDFLTITSSLOPEPFATYFCHQHSPLTFGQGTKEVKTVAAPS 120
DB 83 ESGVDRFRITGSGSGTDFLTITSSLOPEPFATYFCHQHSPLTFGQGTKEVKTVAAPS 142
QY 121 VFIFPPDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQSESVTEODSKDSTYS 180
DB 143 VFIFPPDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQSESVTEODSKDSTYS 202
QY 181 LSSITLTSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 220
DB 203 LSSITLTSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 242

RESULT 2
AAU80039 standard; Protein; 242 AA.

AC AAU80039;

DT 15-JUL-2002 (first entry)

DE HMFG1 Fab/Caspase-3 fusion protein.

KW Caspase-3; HMFG-1; human; milk fat globule membrane; apoptosis;
KW cancer; cytotoxic.

OS Homo sapiens.
OS Synthetic.

PN GB2360772-A.

PD 03-OCT-2001.

PF 28-MAR-2001; 2001GB-0007725.

PR 28-MAR-2000; 2000GB-0007343.

PA (ANTI-) ANTISOMA RES LTD.

PI Epenetos AA;

DR WPI; 2001-640889/74.

DR N-PSDB; ABK49929.

PT New compounds comprising a mediator portion capable of recognising a

PT target cell-specific molecule, and a cytotoxic portion consisting of
PT caspase, useful for treating a disease associated with the dysfunction
PT of cells, e.g. cancer -

XX Disclosure; Fig 3; 85pp; English.

XX The invention relates to compounds comprising a target cell-specific
CC portion or a mediator portion capable of recognising a target cell-
CC specific molecule, and a cytotoxic portion. The compounds are
CC characterised in that the cytotoxic second portion is a constitutively
CC active caspase or has substantially the same apoptosis-inducing activity
CC as the caspases. The compounds and compositions comprising the compounds
CC are useful in medicine, particularly useful in the preparation of a
CC medicament for treating a disease associated with the dysfunction of a
CC population of cells, such as cancer in a human. The present
CC sequence represents the amino acid sequence of the HMFG1 Fab/Caspase-3
CC fusion protein compound of the invention.

XX Sequence 242 AA;

Query Match 92.6%; Score 1057; DB 22; Length 242;
Best Local Similarity 92.7%; Pred. No. 1.4e-57;
Matches 204; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

QY 1 DIQMTQSPSTLSASVGDRTVITCKSSQSLNNSNQNYLAWYQKPKAKPLLYFPASTR 60
DB 23 DIQMTQSPSTLSASVGDRTVITCKSSQSLNNSNQNYLAWYQKPKAKPLLYFMASTR 82
QY 61 ESGVDRFRITGSGSGTDFLTITSSLOPEPFATYFCHQHSPLTFGQGTKEVKTVAAPS 120
DB 83 ESGVDRFRITGSGSGTDFLTITSSLOPEPFATYFCHQHSPLTFGQGTKEVKTVAAPS 142
QY 121 VFIFPPDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQSESVTEODSKDSTYS 180
DB 143 VFIFPPDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQSESVTEODSKDSTYS 202
QY 181 LSSITLTSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 220
DB 203 LSSITLTSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 242

RESULT 3
AAU80338 standard; Protein; 242 AA.

AC AAU80338;

DT 15-JUL-2002 (first entry)

DE Human milk fat globulin 1 (HMFG1) Fab/Caspase 1 fusion protein #2.

KW Human; milk fat globulin 1 Fab/Caspase 1; HMFG1; cytotoxic;
KW apoptosis-inducing; breast cancer; ovarian cancer; lung cancer;
KW stomach cancer; intestinal cancer; blood cancer; fusion protein;
KW tumour cell antigen.

OS Chimeric - Homo sapiens.
OS Chimeric - Synthetic.

PN GB2360771-A.

PD 03-OCT-2001.

PF 28-MAR-2000; 2000GB-0007343.

PR 28-MAR-2000; 2000GB-0007343.

PA (ANTI-) ANTISOMA RES LTD.

PI Epenetos AA;

DR WPI; 2001-640888/74.

DR N-PSDB; ABK50713.

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 31, 2003, 10:32:16 ; Search time 17.0504 Seconds

(without alignments)
2588.856 Million cell updates/sec

Title: US-09-917-410-5

Perfect score: 1142

Sequence: 1 D1QMTQSPETLSASVGRVT.....EYTHQGLSRVTSFNRGEC 220

Scoring table: BLOSUM62

Searched: 733937 seqs, 200641211 residues

Total number of hits satisfying chosen parameters: 733937

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: Listing first 45 summaries

Published Applications AA:*

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3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

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18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1057	92.6	239	10	US-09-825-012-9
3	1011	88.5	240	12	US-10-159-006-36
4	1009	88.4	214	15	US-10-153-382-19
5	1003	87.8	240	9	US-09-799-514-8
6	1000	87.6	242	11	US-09-423-299-3
7	1000	87.6	242	11	US-09-726-258-62
8	1000	87.6	220	10	US-09-995-693-1
9	998.5	87.4	220	15	US-10-232-408-1
10	997.5	87.3	242	11	US-09-726-258-51
11	997.5	87.3	219	11	US-09-726-258-72
12	994.5	87.1	242	11	US-09-726-258-56
13	992	86.9	241	15	US-10-821-945-1
14	991	86.8	263	12	US-10-291-265-335
15	991	86.8	214	9	US-09-940-166A-2

15	991	86.8	214	9	US-09-811-384-11	Sequence 11, Appl
17	991	86.8	237	9	US-09-056-160B-100	Sequence 100, App
18	991	86.8	237	9	US-09-940-166A-6	Sequence 6, Appl
19	991	86.8	237	12	US-10-234-671-100	Sequence 100, App
20	991	86.8	237	15	US-10-020-786-10	Sequence 1, Appl
21	991	86.8	237	15	US-10-227-694-1	Sequence 2, Appl
22	991	86.8	491	14	US-10-011-125-2	Sequence 2, Appl
23	990	86.7	218	9	US-09-917-410-2	Sequence 2, Appl
24	988.5	86.6	213	12	US-10-281-479A-74	Sequence 74, Appl
25	988.5	86.6	213	12	US-10-275-180A-74	Sequence 74, Appl
26	988.5	86.6	213	12	US-10-286-132A-74	Sequence 74, Appl
27	988.5	86.6	239	10	US-09-249-011A-22	Sequence 22, Appl
28	988	86.5	214	12	US-10-356-974-1	Sequence 1, Appl
29	988	86.5	214	12	US-10-423-299-1	Sequence 1, Appl
30	988	86.5	214	15	US-10-253-366-1	Sequence 1, Appl
31	988	86.5	214	15	US-10-316-694-1	Sequence 1, Appl
32	988	86.5	218	9	US-09-802-077-9	Sequence 9, Appl
33	988	86.5	218	9	US-09-802-096-9	Sequence 9, Appl
34	988	86.5	218	9	US-09-920-171-13	Sequence 13, Appl
35	988	86.5	218	11	US-09-925-179-9	Sequence 9, Appl
36	988	86.5	218	12	US-10-113-996-13	Sequence 13, Appl
37	988	86.5	220	12	US-10-159-006-17	Sequence 17, Appl
38	988	86.5	240	12	US-10-159-006-28	Sequence 28, Appl
39	985.5	86.3	213	12	US-10-281-479A-73	Sequence 73, Appl
40	985.5	86.3	213	12	US-10-275-180A-73	Sequence 73, Appl
41	985.5	86.3	213	12	US-10-286-132A-73	Sequence 73, Appl
42	984	86.2	212	12	US-10-320-231A-77	Sequence 77, Appl
43	984	86.2	236	10	US-09-859-053-30	Sequence 30, Appl
44	984	86.2	237	15	US-10-020-786-8	Sequence 8, Appl
45	984	86.2	237	15	US-10-227-694-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-09-917-410-5
Patent No. US20020098183A1
GENERAL INFORMATION:

APPLICANT: MARTIN, Ulrich; HASELBECK, Anton; SCHUMACHER, Guenther;

TITLE OF INVENTION: ANTI-L-SELECTIN ANTIBODIES FOR PREVENTION OF MULTIPLE ORGAN FAILURE AFTER POLYTRAUMA AND FOR PREVENTION OF ACUTE ORGAN DAMAGE AFTER EXTRACORPOREAL BLOOD CIRCULATION

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Felte & Lynch

STREET: 805 Third Avenue

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10022

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Computer Disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII, WordPerfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/917,410

FILING DATE: 26-Jul-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/578,953

FILING DATE: <Unknown>

APPLICATION NUMBER: EP 95 114 969.9

ATTORNEY/AGENT INFORMATION:

NAME: Hanson, No. US20020098183A1man D.

REGISTRATION NUMBER: 30,946

REFERENCE/DOCKET NUMBER: BOER 1059-PFF/NDH/SLH

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 688-9200
 TELEFAX: (212) 838-3884
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 220 amino acid residues
 TYPE: amino acid
 TOPOLOGY: linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 5:
 US-09-917-410-5

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 Best Local Similarity 100.0%; Pred. No. 1,7e-69;
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 DB 1 DIQMTQSPSTLSASVGRVTITCKSSQSLNNSNOKNYLAWYQOKPGKAPKLLVYFASTR 60
 QY 61 ESGVDRFISGSGTDFTLTISLQPEDFATYFCHQHYSTPLTFQGTKEVKKTVAAAPS 120
 |||
 DB 61 ESGVDRFISGSGTDFTLTISLQPEDFATYFCHQHYSTPLTFQGTKEVKKTVAAAPS 120
 QY 121 VFIFPPSDQKSGTASVCLNNFYPREAKYQKVDNALQSGNSQESVTEQDSKDSITYS 180
 |||
 DB 121 VFIFPPSDQKSGTASVCLNNFYPREAKYQKVDNALQSGNSQESVTEQDSKDSITYS 180
 QY 181 LSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 220
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 DB 181 LSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 220

RESULT 2

US-09-825-012-9
 ; Sequence 9, Application US/09825012
 ; Patent No. US20020122798A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Young, Robert
 ; TITLE OF INVENTION: Compounds for Targeting
 ; FILE REFERENCE: 43191-256808
 ; CURRENT APPLICATION NUMBER: US/09/825,012
 ; CURRENT FILING DATE: 2001-04-03
 ; PRIOR APPLICATION NUMBER: US 60/237,159
 ; PRIOR FILING DATE: 2000-10-02
 ; PRIOR APPLICATION NUMBER: GB 0008049.9
 ; PRIOR FILING DATE: 2000-04-03
 ; NUMBER OF SEQ ID NOS: 102
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 9
 ; LENGTH: 239
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Humanised HMF-1 light chain
 US-09-825-012-9

Query Match 92.6%; Score 1057; DB 10; Length 239;
 Best Local Similarity 92.7%; Pred. No. 9e-64;
 Matches 204; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

QY 1 DIQMTQSPSTLSASVGRVTITCKSSQSLNNSNOKNYLAWYQOKPGKAPKLLVYFASTR 60
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 DB 80 ESGVDRFISGSGTDFTLTISLQPEDFATYFCHQHYSTPLTFQGTKEVKKTVAAAPS 139
 QY 121 VFIFPPSDQKSGTASVCLNNFYPREAKYQKVDNALQSGNSQESVTEQDSKDSITYS 180
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 DB 140 VFIFPPSDQKSGTASVCLNNFYPREAKYQKVDNALQSGNSQESVTEQDSKDSITYS 199
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DB 200 LSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 239

RESULT 3

US-10-159-006-36
 ; Sequence 36, Application US/10159006
 ; Publication No. US20030143229A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Park, John E.
 ; APPLICANT: Garin-Chesa, Pilar
 ; APPLICANT: Bamberger, Uwe
 ; APPLICANT: Leger, Olivier
 ; APPLICANT: Saldanha, Jose W.
 ; APPLICANT: Rettig, Wolfgang J.
 ; TITLE OF INVENTION: PAPA-specific Antibody with Improved Productibility
 ; FILE REFERENCE: 0652,1890002
 ; CURRENT APPLICATION NUMBER: US/10/159,006
 ; CURRENT FILING DATE: 2002-06-03
 ; PRIOR APPLICATION NUMBER: US 09/301,593
 ; PRIOR FILING DATE: 1999-04-29
 ; PRIOR APPLICATION NUMBER: EP 98107925.4
 ; PRIOR FILING DATE: 1998-04-30
 ; PRIOR APPLICATION NUMBER: US 60/086,049
 ; PRIOR FILING DATE: 1998-05-18
 ; NUMBER OF SEQ ID NOS: 108
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 36
 ; LENGTH: 240
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-159-006-36

Query Match 88.5%; Score 1011; DB 12; Length 240;
 Best Local Similarity 87.7%; Pred. No. 1.1e-60;
 Matches 193; Conservative 12; Mismatches 15; Indels 0; Gaps 0;

QY 1 DIQMTQSPSTLSASVGRVTITCKSSQSLNNSNOKNYLAWYQOKPGKAPKLLVYFASTR 60
 |||
 DB 21 DIQMTQSPSTLSASVGRVTITCKSSQSLNNSNOKNYLAWYQOKPGKAPKLLVYFASTR 80
 QY 61 ESGVDRFISGSGTDFTLTISLQPEDFATYFCHQHYSTPLTFQGTKEVKKTVAAAPS 120
 |||
 DB 81 ESGVDRFISGSGTDFTLTISLQPEDFATYFCHQHYSTPLTFQGTKEVKKTVAAAPS 140
 QY 121 VFIFPPSDQKSGTASVCLNNFYPREAKYQKVDNALQSGNSQESVTEQDSKDSITYS 180
 |||
 DB 141 VFIFPPSDQKSGTASVCLNNFYPREAKYQKVDNALQSGNSQESVTEQDSKDSITYS 200
 QY 181 LSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 220
 |||
 DB 201 LSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 240

RESULT 4

US-10-153-382-19
 ; Sequence 19, Application US/10153382
 ; Publication No. US20030086930A1
 ; GENERAL INFORMATION:
 ; APPLICANT: PRIZER PRODUCTS INC.
 ; TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES
 ; FILE REFERENCE: PC23019A
 ; CURRENT APPLICATION NUMBER: US/10/153,382
 ; CURRENT FILING DATE: 2002-05-22
 ; PRIOR APPLICATION NUMBER: 60/293042
 ; PRIOR FILING DATE: 2001-05-23
 ; NUMBER OF SEQ ID NOS: 39
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 19
 ; LENGTH: 214
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-153-382-19

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 31, 2003, 10:29:11 ; Search time 8.2769 Seconds

(without alignments)
1124.623 Million cell updates/sec

Title: US-09-917-410-5

Perfect score: 1142

Sequence: 1 DIWMTQSPSTLSASVGDRTV.....EVTHQGLSSPVTKSPNRGEC 220

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Issued Patents AA:*

1: /cgn2_6/ptodata/1/1aa/5A.COMB.dep:*

2: /cgn2_6/ptodata/1/1aa/5B.COMB.dep:*

3: /cgn2_6/ptodata/1/1aa/6A.COMB.dep:*

4: /cgn2_6/ptodata/1/1aa/6B.COMB.dep:*

5: /cgn2_6/ptodata/1/1aa/PTUS.COMB.dep:*

6: /cgn2_6/ptodata/1/1aa/backfile1.dep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1011	88.5	240	4 US-09-301-593-36	Sequence 36, Appl
2	1000.5	87.6	242	3 US-09-027-449-62	Sequence 62, Appl
3	1000.5	87.6	242	3 US-09-026-985-62	Sequence 62, Appl
4	1000.5	87.6	242	4 US-09-121-952A-62	Sequence 62, Appl
5	1000.5	87.6	242	4 US-09-234-340A-62	Sequence 62, Appl
6	1000	87.6	220	3 US-08-952-235-1	Sequence 1, Appl
7	1000	87.6	220	4 US-09-669-971-1	Sequence 1, Appl
8	998.5	87.4	242	3 US-09-027-449-51	Sequence 51, Appl
9	998.5	87.4	242	3 US-08-804-44A-51	Sequence 51, Appl
10	998.5	87.4	242	3 US-09-026-985-51	Sequence 51, Appl
11	998.5	87.4	242	4 US-09-121-952A-51	Sequence 51, Appl
12	998.5	87.4	242	4 US-09-234-340A-51	Sequence 51, Appl
13	997.5	87.3	219	3 US-09-027-449-72	Sequence 72, Appl
14	997.5	87.3	219	3 US-09-026-985-72	Sequence 72, Appl
15	997.5	87.3	219	4 US-09-121-952A-72	Sequence 72, Appl
16	997.5	87.3	219	4 US-09-234-340A-72	Sequence 72, Appl
17	997.5	87.3	242	3 US-09-027-449-56	Sequence 56, Appl
18	997.5	87.3	242	3 US-08-804-44A-56	Sequence 56, Appl
19	997.5	87.3	242	3 US-09-026-985-56	Sequence 56, Appl
20	997.5	87.3	242	4 US-09-121-952A-56	Sequence 56, Appl
21	997.5	87.3	242	4 US-09-234-340A-56	Sequence 56, Appl
22	996	87.2	214	2 US-07-934-373C-39	Sequence 39, Appl
23	996	87.2	214	2 US-08-437-642B-39	Sequence 39, Appl
24	996	87.2	214	5 PCT-US93-07832-39	Sequence 39, Appl
25	991	86.8	214	2 US-07-934-373C-40	Sequence 40, Appl
26	991	86.8	214	2 US-08-788-800-11	Sequence 11, Appl
27	991	86.8	214	3 US-08-437-642B-40	Sequence 40, Appl

28	991	86.8	214	3 US-09-097-309-2	Sequence 2, Appl
29	991	86.8	214	3 US-09-097-171A-2	Sequence 2, Appl
30	991	86.8	214	4 US-09-460-587-2	Sequence 2, Appl
31	991	86.8	214	5 PCT-US93-07832-40	Sequence 40, Appl
32	991	86.8	233	2 US-07-934-373C-25	Sequence 25, Appl
33	991	86.8	233	3 US-08-437-642B-25	Sequence 25, Appl
34	991	86.8	233	4 US-08-146-206C-25	Sequence 25, Appl
35	991	86.8	233	5 PCT-US93-07832-25	Sequence 25, Appl
36	991	86.8	237	3 US-09-097-309-6	Sequence 6, Appl
37	991	86.8	237	3 US-09-097-171A-10	Sequence 10, Appl
38	991	86.8	237	3 US-09-422-112B-2	Sequence 2, Appl
39	991	86.8	237	3 US-09-607-756-2	Sequence 2, Appl
40	991	86.8	237	4 US-09-460-587-6	Sequence 6, Appl
41	990	86.7	214	1 US-08-458-516-12	Sequence 12, Appl
42	990	86.7	218	5 PCT-US96-13152-2	Sequence 2, Appl
43	989.5	86.6	241	2 US-07-916-098A-56	Sequence 56, Appl
44	988	86.5	214	4 US-09-679-397-1	Sequence 1, Appl
45	988	86.5	214	4 US-09-680-148-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-09-301-593-36
; Sequence 36, Application US/09301593A
; Patent No. 6455677
; GENERAL INFORMATION:
; APPLICANT: Park, John E.
; APPLICANT: Garin-Chesa, Pilar
; APPLICANT: Bamberger, Iwe
; APPLICANT: Legier, Olivier
; APPLICANT: Saldanha, Jose W.
; APPLICANT: Retig, Wolfgang J.
; TITLE OF INVENTION: PAP-specific Antibody with Improved Productibility
; FILE REFERENCE: 0652.1890001
; CURRENT APPLICATION NUMBER: US/09/301.593A
; CURRENT FILING DATE: 1999-04-29
; EARLIER APPLICATION NUMBER: EP 98107925.4
; EARLIER FILING DATE: 1998-04-30
; EARLIER APPLICATION NUMBER: US 60/086.049
; EARLIER FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 36
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-301-593-36

Query Match 88.5%; Score 1011; DB 4; Length 240;
Best Local Similarity 87.7%; Pred. No. 7,3e-78;
Matches 193; Conservative 12; Mismatches 15; Indels 0; Gaps 0;

QY	1	DIWMTQSPSTLSASVGDRTVITTKSSQSLNNSNQNYLAWYQKPKAKRLVYFASTR	60
DB	21	DIWMTQSPDLSAVSLGRATINCKSSQSLYSHRNQNYLAWYQKPKPKLIFMASTR	80
QY	61	ESGVPRDFISSGSGTPTLTITSSLOPEDRTYCHQHYSTPLTFGQTKVEKRTVAPS	120
DB	81	ESGVPRDFSSGSGTPTLTITSSLOQEDVAVVYCOQYFSLTFGQTKVEIKRTVAPS	140
QY	121	VFIFFPEDQLKSGTASVCLNNFYPRKAVQMKVDNALQSGNSQSESVTEQDSKOSTYS	180
DB	141	VFIFFPEDQLKSGTASVCLNNFYPRKAVQMKVDNALQSGNSQSESVTEQDSKOSTYS	200
QY	181	LSSTLTLSKADYKHKRYACEVTHQGLSSPVTKSPNRGEC	220
DB	201	LSSTLTLSKADYKHKRYACEVTHQGLSSPVTKSPNRGEC	240

RESULT 2
US-09-027-449-62

Sequence 62, Application US/09027449
Patent No. 6025158
GENERAL INFORMATION:
APPLICANT: Gonzalez, Tania R.
APPLICANT: Leon, Steven R.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/027,449
FILING DATE: 20-Feb-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/074,330
FILING DATE: 22-Jan-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/038,664
FILING DATE: 21-Feb-1997
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085R3-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 242 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-027-449-62
Query Match 87.6%; Score 1000.5; DB 3; Length 242;
Best Local Similarity 88.6%; Pred. No. 5.7e-77;
Matches 195; Conservative 8; Mismatches 16; Indels 1; Gaps 1;
QY 1 DIQMTQSPSTLSASVGRVTITCKSSQSLINSSNQKYLAWYQKPKAPKLLVYFASTR 60
DB 24 DIQMTQSPSSLSASVGRVTITCKSSQSLINSSNQKYLAWYQKPKAPKLLVYFASTR 82
QY 61 ESVGPRFRTIGSGSGTDFLTITSSLOPEDFATYFCHQHYSTPLTFGQGTKEVETVAAPS 120
DB 83 FSGVPSRFSFGSGSGTDFLTITSSLOPEDFATYFCHQHYSTPLTFGQGTKEVETVAAPS 142
QY 121 VFIFPPSDQQLKSGTASVCLNNFYPREAKYQKVNALQSGNSQSVTEQDSKDYTS 180
DB 143 VFIFPPSDQQLKSGTASVCLNNFYPREAKYQKVNALQSGNSQSVTEQDSKDYTS 202
QY 181 LSTLTLSKADYEKHKYVACEVTHQGLSPVTKSFNRGEC 220
DB 203 LSTLTLSKADYEKHKYVACEVTHQGLSPVTKSFNRGEC 242

RESULT 3
US-09-026-985-62
Sequence 62, Application US/09026985
Patent No. 6133426
GENERAL INFORMATION:
APPLICANT: Gonzalez, Tania R.
APPLICANT: Leon, Steven R.

APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/026,985
FILING DATE: 20-Feb-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085R3-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 242 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-026-985-62
Query Match 87.6%; Score 1000.5; DB 3; Length 242;
Best Local Similarity 88.6%; Pred. No. 5.7e-77;
Matches 195; Conservative 8; Mismatches 16; Indels 1; Gaps 1;
QY 1 DIQMTQSPSTLSASVGRVTITCKSSQSLINSSNQKYLAWYQKPKAPKLLVYFASTR 60
DB 24 DIQMTQSPSSLSASVGRVTITCKSSQSLINSSNQKYLAWYQKPKAPKLLVYFASTR 82
QY 61 ESVGPRFRTIGSGSGTDFLTITSSLOPEDFATYFCHQHYSTPLTFGQGTKEVETVAAPS 120
DB 83 FSGVPSRFSFGSGSGTDFLTITSSLOPEDFATYFCHQHYSTPLTFGQGTKEVETVAAPS 142
QY 121 VFIFPPSDQQLKSGTASVCLNNFYPREAKYQKVNALQSGNSQSVTEQDSKDYTS 180
DB 143 VFIFPPSDQQLKSGTASVCLNNFYPREAKYQKVNALQSGNSQSVTEQDSKDYTS 202
QY 181 LSTLTLSKADYEKHKYVACEVTHQGLSPVTKSFNRGEC 220
DB 203 LSTLTLSKADYEKHKYVACEVTHQGLSPVTKSFNRGEC 242

RESULT 4
US-09-121-952A-62
Sequence 62, Application US/09121952A
Patent No. 6458355
GENERAL INFORMATION:
APPLICANT: Genentech, Inc., Heel, Vanessa
APPLICANT: Koumenda, Iphigenia
APPLICANT: Leon, Steven R.
APPLICANT: Presta, Leonard G.
APPLICANT: Shantokh, Zahra
APPLICANT: Zapata, Gerardo A.
TITLE OF INVENTION: METHODS OF TREATING INFLAMMATORY DISEASES
TITLE OF INVENTION: WITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER CONJUGATES
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using SW model

Run on: December 31, 2003, 10:29:11 ; Search time 17.1919 Seconds

(without alignments)
2506.043 Million cell updates/sec

Title: US-09-917-410-6

Perfect score: 2389

Sequence: 1 QVQLVQSGAEVKKPGSSVKV.....MHALHNHYTQKSLSLSLGK 448

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

PIR 76:*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1743	73.0	327	1 G4HU	Ig gamma-4 chain C
2	1605.5	67.2	326	1 G2HU	Ig gamma-2 chain C
3	1590.5	66.6	330	1 G4HU	Ig gamma-1 chain C
4	1585	66.3	377	2 A60764	Ig gamma-3 chain C
5	1575	65.9	377	2 A23511	Ig gamma-3 chain C
6	1531	64.1	469	2 S37483	Ig gamma-2a chain C
7	1520.5	63.6	446	2 S40295	Ig gamma-2a chain C
8	1492.5	62.5	474	1 G2K811	Ig gamma-2b chain C
9	1467.5	61.4	470	2 S22080	Ig heavy chain pre
10	1448.5	60.6	472	2 S31459	Ig gamma-1 chain -
11	1433	60.0	444	2 PC4436	monoclonal antibod
12	1410	59.0	475	2 S01321	Ig gamma-2b chain C
13	1327.5	55.6	374	2 S69339	Ig heavy chain V r
14	1289.5	54.0	328	2 I47159	Ig gamma-2a chain C
15	1283.5	53.7	328	2 I47160	Ig gamma-2b chain C
16	1264.5	52.9	328	2 I47161	Ig gamma-3 chain C
17	1240.5	51.9	328	2 I47158	Ig gamma-1 chain C
18	1199	50.2	323	1 GHRB	Ig gamma-1 chain C
19	1162	48.6	329	1 G2GP	Ig gamma-2 chain C
20	1147	48.0	308	2 C30554	Ig gamma-2 chain C
21	1139.5	47.3	255	4 S31866	Ig heavy chain C r
22	1129.5	47.0	334	2 PT0207	Ig gamma-1 chain C
23	1124	46.8	326	2 PS0018	Ig gamma-2b chain C
24	1118.5	46.4	289	1 G3HUM1	Ig gamma-1 chain C
25	1108.5	46.4	329	2 S00847	Ig gamma-3 heavy c
26	1108	46.4	329	2 S00847	Ig gamma-2c heavy c
27	1106.5	46.3	324	1 GIMS	Ig gamma-1 chain C
28	1106.5	46.3	330	1 G2MSA	Ig gamma-2a chain C
29	1103	46.2	327	2 S06611	Ig gamma-2 chain C

ALIGNMENTS

RESULT 1

G4HU

Ig gamma-4 chain C region - human

C/Species: Homo sapiens (man)

C/Date: 02-Apr-1982 #sequence revision 02-Apr-1982 #ext_change 16-Jul-1999

C/Accession: A90249; A90249; A02150

R/Elision: U.; Buxbaum, U.; Hood, L.

DNA 1, 11-18, 1981

A/Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.

A/Reference number: A90933; PMID:83157104; PMID:6299662

A/Accession: A90933

A/Molecule type: DNA

A/Residues: 1-327 <EL>

A/Note: The sequence was determined from the germline gene

Biochem. J. 117, 33-47, 1970

A/Title: Human immunoglobulin subclones. Partial amino acid sequence of the constant

A/Reference number: A90249; PMID:70207560; PMID:4192699

A/Accession: A90249

A/Molecule type: protein

A/Residues: 1-30; 81-326 <PIN>

C/Genetics:

A/Gene: GDB:IGHG4

A/Cross-references: GDB:119340; OMIM:147130

A/Map position: 14q32.33-14q32.33

A/Introns: 99/1, 111/1, 221/1

C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into 1a

C/Superfamily: immunoglobulin C region; immunoglobulin homology

C/Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin

F:20-85/Domain: immunoglobulin homology <IM1>

F:134-203/Region: hinge

F:134-203/Domain: immunoglobulin homology <IM2>

F:240-307/Domain: immunoglobulin homology <IM3>

F:27-83, 141-201, 247-305/Disulfide bonds: #status experimental

F:106, 109/Disulfide bonds: interchain (to heavy chain) #status experimental

F:177/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 73.0%; Score 1743; DB 1; Length 327;

Best local similarity 100.0%; Pred. No. 26-93;

Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	122	ASTGSPVFPAPCRSTSESTALGLVVDYDPPEPTVWNSGALTSVHTPPAVIQSS	181
Db	1	ASTGSPVFPAPCRSTSESTALGLVVDYDPPEPTVWNSGALTSVHTPPAVIQSS	60
Qy	182	GLVSLSSVTVPPSSSLGKTTCNVDPKPSNTKVDKVESKYPGPGSCAPAFGLGSPV	241
Db	61	GLVSLSSVTVPPSSSLGKTTCNVDPKPSNTKVDKVESKYPGPGSCAPAFGLGSPV	120
Qy	242	PLFPKPKDLMISRTPEVTCTVVDVDSQEDPEVQFMVYDGVHNAKTKPREEOFNSTY	301

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Db 121 FLPPKPKDTLMIRTPPEVTQVVDVSDGEDEPEVGFNMYVDGEVHNAKTKPREQFNSTY 180
Oy 302 RVSVSLTVLHODWLNKGEYKCKVSNKGLPSSIEKTIISAKQCPPEPOVYTLPPSQEEMTK 361
Db 181 RVSVSLTVLHODWLNKGEYKCKVSNKGLPSSIEKTIISAKQCPPEPOVYTLPPSQEEMTK 240
Oy 362 NOVSLTCLVKGFPSPDIAVEMESNGQPENNYKTPPVLDSDGSFFLYSRLTVDSKSRMQEG 421
Db 241 NOVSLTCLVKGFPSPDIAVEMESNGQPENNYKTPPVLDSDGSFFLYSRLTVDSKSRMQEG 300
Oy 422 NVFSCSVHMEALHNHYTKSLSLSGK 448
Db 301 NVFSCSVHMEALHNHYTKSLSLSGK 327

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RESULT 2

G2HU

Ig gamma-2 chain C region - human

C/Species: Homo sapiens (man)

C/Date: 30-Apr-1981 #sequence revision 13-Jun-1983 #ext_change 21-Jul-2000

C/Accession: A93906; A92809; A90752; A93132; A02148

R.Elliison, J.; Hood, L.

Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982

A/Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain cor

A/Reference number: A93906; PMID:82197621; PMID:6804948

A/Accession: A93906

A/Molecule type: DNA

A/Residues: 1-326 <EHL>

A/Cross-references: GB:V00554; GB:J00230; NID:932759; PIDN:CAB58438.1; PMID:6066056

A/Note: Lys-326 is probably removed posttranslationally

R.Wang, A.C.; Tung, E.; Pudenberg, H.H.

J. Immunol. 125, 1048-1054, 1980

A/Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and f

A/Reference number: A92809; PMID:81007873; PMID:6774012

A/Accession: A92809

A/Molecule type: protein

A/Residues: 1-19, 'Q', '21-57', 'Z', '59', 'A', '61-193', 'D', '195-325 <WAN>

A/Note: Trp-156 is at or near the complement-binding site

R.Comnell, G.B.; Parr, D.M.; Hofmann, T.

Can. J. Biochem. 57, 758-767, 1979

A/Title: The amino acid sequences of the three heavy chain constant region domains of a

A/Reference number: A90752; PMID:8001357; PMID:113060

A/Accession: A90752

A/Molecule type: protein

A/Residues: 1-24, 'E', '26-57', 'EV', '60-85', '132-171', 'ZZZ', '175', 'B', '177-193', 'D', '195-196', 'Q', '198-

A/Note: this sequence has since been revised

R.Hofmann, T.; Parr, D.M.

Mol. Immunol. 16, 923-925, 1979

A/Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin g

A/Reference number: A93132; PMID:80114419; PMID:118920

A/Accession: A93132

A/Molecule type: protein

A/Residues: 238-275 <HOF>

R.Hofmann, T.; Parr, D.M.

Submitted to the Atlas March 1980

A/Reference number: A94591

A/Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268

A/Note: the revised sequence differs from that shown in having 60-Ala and in the amidact

ned

R.Milstein, C.; Frangione, B.

Biochem. J. 121, 217-225, 1971

A/Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.

A/Reference number: A90253; PMID:7203350; PMID:4940472

A/Accession: A90253

A/Molecule type: protein

A/Residues: 238-275 <HOF>

R.Hofmann, T.; Parr, D.M.

Submitted to the Atlas March 1980

```

C/Genetics:
A/Gene: GDB:IGHG2
A/Cross-references: GDB:119338; OMIM:147110
A/Map position: 14q32.33-14q32.33
A/Complex: An immunoglobulin heterotrimer subunit consists of two identical light (k)
chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 16
C/Superfamily: immunoglobulin C region; immunoglobulin homology
C/Keywords: duplication; glycoprotein; heterotrimer; immunoglobulin
F/20-85/Domain: immunoglobulin homology <IM1>
F/133-202/Domain: immunoglobulin homology <IM2>
F/133-202/Domain: immunoglobulin homology <IM3>
F/14/Disulfide bonds: interchain (to light chain) #status experimental
F/27-83,140-200,246-304/Disulfide bonds: #status experimental
F/102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F/176/Binding site: carbohydrate (Asn) (covalent) #status predicted

```

Query Match 67.2%; Score 1605.5; DB 1; Length 326;

Best Local Similarity 92.4%; Pred. No. 1.7e-85; Indels 1; Gaps 1;

Matches 302; Conservative 10; Mismatches 14;

```

Oy 122 ASTKPSVFPAPCSRSTSESTALGCLVNDYPEPEVTVSMNSGALTSGVHTPPAVIQSS 181
Db 1 ASTKPSVFPAPCSRSTSESTALGCLVNDYPEPEVTVSMNSGALTSGVHTPPAVIQSS 60
Oy 182 GLVSLSSVTVTPSSSLGCTTYTCNVDHKPSNTKYDKRVESKGPCCSCAPERIGSPV 241
Db 61 GLVSLSSVTVTPSSSLGCTTYTCNVDHKPSNTKYDKRVESKGPCCSCAPERIGSPV 119
Oy 242 FLPPKPKDTLMIRTPPEVTQVVDVSDGEDEPEVGFNMYVDGEVHNAKTKPREQFNSTY 301
Db 242 FLPPKPKDTLMIRTPPEVTQVVDVSDGEDEPEVGFNMYVDGEVHNAKTKPREQFNSTY 179
Oy 120 FLPPKPKDTLMIRTPPEVTQVVDVSDGEDEPEVGFNMYVDGEVHNAKTKPREQFNSTY 179
Db 120 FLPPKPKDTLMIRTPPEVTQVVDVSDGEDEPEVGFNMYVDGEVHNAKTKPREQFNSTY 179
Oy 302 RVSVSLTVLHODWLNKGEYKCKVSNKGLPSSIEKTIISAKQCPPEPOVYTLPPSQEEMTK 361
Db 302 RVSVSLTVLHODWLNKGEYKCKVSNKGLPSSIEKTIISAKQCPPEPOVYTLPPSQEEMTK 239
Oy 180 RVSVSLTVLHODWLNKGEYKCKVSNKGLPSSIEKTIISAKQCPPEPOVYTLPPSQEEMTK 239
Db 180 RVSVSLTVLHODWLNKGEYKCKVSNKGLPSSIEKTIISAKQCPPEPOVYTLPPSQEEMTK 239
Oy 362 NOVSLTCLVKGFPSPDIAVEMESNGQPENNYKTPPVLDSDGSFFLYSRLTVDSKSRMQEG 421
Db 362 NOVSLTCLVKGFPSPDIAVEMESNGQPENNYKTPPVLDSDGSFFLYSRLTVDSKSRMQEG 299
Oy 240 NOVSLTCLVKGFPSPDIAVEMESNGQPENNYKTPPVLDSDGSFFLYSRLTVDSKSRMQEG 299
Db 240 NOVSLTCLVKGFPSPDIAVEMESNGQPENNYKTPPVLDSDGSFFLYSRLTVDSKSRMQEG 299
Oy 422 NVFSCSVHMEALHNHYTKSLSLSGK 448
Db 422 NVFSCSVHMEALHNHYTKSLSLSGK 326
Oy 300 NVFSCSVHMEALHNHYTKSLSLSGK 326
Db 300 NVFSCSVHMEALHNHYTKSLSLSGK 326

```

RESULT 3

GHHD

Ig gamma-1 chain C region - human

C/Species: Homo sapiens (man)

C/Date: 31-Jan-1981 #sequence revision 18-Aug-1982 #ext_change 16-Jul-1999

C/Accession: A93433; S36861; S33887; B90563; A90564; B91668; A91723; A02146

R.Elliison, J.W.; Berson, B.J.; Hood, L.E.

Nucleic Acids Res. 10, 4071-4079, 1982

A/Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.

A/Reference number: A93433; PMID:82274238; PMID:6287432

A/Accession: A93433

A/Molecule type: DNA

A/Residues: 1-330 <EHL>

A/Cross-references: EMBL:Z17370

A/Note: this sequence has the Gln(17) allotypic marker, 97-Lys, and the Gln(1) markers,

R.Harris, L.J.

submitted to the EMBL Data Library, October 1992

A/Reference number: S33904

A/Accession: S36861

A/Molecule type: DNA

A/Residues: 2-330 <HAR>

A/Cross-references: EMBL:Z17370

R.Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.

Cell 29, 671-679, 1982

A/Title: Structure of human immunoglobulin gamma genes: implications for evolution of a

A/Reference number: S33887; PMID:83001943; PMID:6811139

A/Accession: S33887

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 31, 2003, 10:29:10 ; Search time 10.7871 Seconds

(without alignments)
1953.078 Million cell updates/sec

Title: US-09-917-410-6

Perfect score: 2389

Sequence: 1 QVQLVQSGAEVKKPGSSVKV.....MEEALHNHYTKSLSLGK 448

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1743	73.0	327	1 GC4_HUMAN	P01861 homo sapien
2	1605.5	67.2	326	1 GC2_HUMAN	P01859 homo sapien
3	1590.5	66.6	330	1 GC1_HUMAN	P01857 homo sapien
4	1199	50.2	323	1 GC_FABIT	P01870 oryctolagus
5	1162	48.6	329	1 GC2_CAVPO	P01862 cavia porce
6	1124	47.0	333	1 GC3_RAT	P20761 rattus norv
7	1118.5	46.8	326	1 GC1_RAT	P20759 rattus norv
8	1113.5	46.4	290	1 GC3_HUMAN	P01860 homo sapien
9	1108	46.4	329	1 GC3_RAT	P20762 rattus norv
10	1106.5	46.3	324	1 GC1_MOUSE	P01868 mus musculu
11	1106.5	46.3	330	1 GC4_MOUSE	P01863 mus musculu
12	1101.5	46.1	393	1 GC1_MOUSE	P01869 mus musculu
13	1101.5	46.1	399	1 GC4_MOUSE	P01865 mus musculu
14	1099	46.0	335	1 GC4_MOUSE	P01864 mus musculu
15	1098.5	46.0	329	1 GC3_MOUSE	P22436 mus musculu
16	1090.5	45.6	398	1 GC3_MOUSE	P03987 mus musculu
17	1084.5	45.4	322	1 GC4_RAT	P20760 rattus norv
18	1054.5	44.1	336	1 GC3_MOUSE	P01866 mus musculu
19	1049.5	43.9	405	1 GC4_MOUSE	P01867 mus musculu
20	496	20.8	429	1 BPC_RAT	P01855 rattus norv
21	482.5	20.2	421	1 BPC_MOUSE	P06336 mus musculu
22	478.5	20.0	428	1 BPC_HUMAN	P01854 homo sapien
23	447.5	18.7	454	1 MUC_HUMAN	P01871 homo sapien
24	441.5	18.5	139	1 HV07_MOUSE	P01751 mus musculu
25	439	18.4	120	1 HV03_MOUSE	P01747 mus musculu
26	434.5	18.2	120	1 HV50_MOUSE	P06329 mus musculu
27	433.5	18.1	457	1 MUC_SUNMU	P20768 suncus muri
28	432.5	18.1	455	1 MUC_MOUSE	P01872 mus musculu
29	431.5	18.1	137	1 HV1_MOUSE	P01755 mus musculu
30	430.5	18.0	450	1 MUC_CANFA	P01874 canis famill
31	426	17.8	458	1 MUC_RABIT	P03988 oryctolagus
32	425	17.8	117	1 HV13_MOUSE	P01757 mus musculu
33	422.5	17.7	476	1 MUCM_MOUSE	P01873 mus musculu

34	422	17.7	454	1 MUC_MESAU	P06337 mesocricetu
35	421	17.6	117	1 HV12_MOUSE	P01756 mus musculu
36	420	17.6	140	1 HV02_MOUSE	P01746 mus musculu
37	416.5	17.4	147	1 HV1C_HUMAN	P01744 homo sapien
38	416	17.4	117	1 HV1B_HUMAN	P01743 homo sapien
39	416	17.4	479	1 MUCM_RABIT	P04221 oryctolagus
40	411.5	17.2	391	1 MUCB_HUMAN	P04220 homo sapien
41	409.5	17.1	114	1 HV00_MOUSE	P01741 mus musculu
42	406	17.0	117	1 HV1G_HUMAN	P23083 mus sapien
43	403.5	16.9	118	1 HV51_MOUSE	P06330 mus musculu
44	402	16.8	121	1 HV01_MOUSE	P01745 mus musculu
45	397	16.6	117	1 HV1A_HUMAN	P01742 homo sapien

ALIGNMENTS

RESULT 1	ID	GC4_HUMAN	STANDARD;	PRT;	327 AA.
AC	P01861;				
DT	21-JUL-1986 (Rel. 01, Created)				
DT	21-JUL-1986 (Rel. 01, Last sequence update)				
DT	15-SEP-2003 (Rel. 42, Last annotation update)				
DE	IG gamma-4 chain C region.				
GN	IGHG4.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	(1)				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=83157104; PubMed=629662;				
RA	Ellison J.W., Buxbaum J.N., Hood L.E.;				
RT	"Nucleotide sequence of a human immunoglobulin C gamma 4 gene.";				
RL	DNA 1:11-18 (1981).				
RN	(2)				
RP	SEQUENCE OF 1-30 AND 81-326.				
RX	MEDLINE=70207560; PubMed=4192699;				
RA	Pink J.R.L., Buttery S.H., de Vries G.M., Milstein C.;				
RT	"Human immunoglobulin subclasses. Partial amino acid sequence of the constant region of a gamma 4 chain.";				
RL	Biochem. J. 117:33-47 (1970).				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@sib.ch).				
CC	or send an email to license@sib.ch .				
CC	EMBL; K01316; AAB59394.1; ALT_INIT.				
DR	PIR; A90933; G4HU.				
DR	PDB; 1ADQ; 16-SEP-98.				
DR	Genew; HGNC:5528; IGHG4.				
DR	MIM; 147130.				
DR	GO; GO:0005624; C:membrane fraction; NAS.				
DR	GO; GO:0003823; F:antigen binding activity; TAG.				
DR	GO; GO:0006955; P:immune response; NAS.				
DR	InterPro; IPR007110; IG-like.				
DR	InterPro; IPR003597; IG-cl.				
DR	InterPro; IPR003006; IG_MHC.				
DR	Pfam; PF00047; I97.3.				
DR	SMART; SM00407; IGc1.2.				
DR	PROSITE; PS50835; IG_LIKE.3.				
DR	PROSITE; PS00290; IG_MHC.2.				
KW	Immunoglobulin domain; Immunoglobulin C region; 3D-structure.				
FT	NON_TER	1			
FT	DOMAIN	1	98		CH1.
FT	DOMAIN	99	110		HINGE.
FT	DOMAIN	111	220		CH2.
FT	DOMAIN	221	327		CH3.

FT DISULFID 14 14 INTERCHAIN (WITH A LIGHT CHAIN).
 FT DISULFID 27 83 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 141 201
 FT DISULFID 247 305
 SQ SEQUENCE 327 AA; 35940 MW; 3EDBD811EF208E7A CRC64;
 Query Match 73.0%; Score 1743; DB 1; Length 327;
 Best Local Similarity 100.0%; Pred. No. 1,1e-111; Indels 0; Gaps 0;
 Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 122 ASTGPEVFLPAPCSRSTSESTALGCLVNDYFPEPVTVSNNGALTSVHTPEAVLQSS 181
 DB 1 ASTGPEVFLPAPCSRSTSESTALGCLVNDYFPEPVTVSNNGALTSVHTPEAVLQSS 60
 QY 182 GLVSLSSVTVPPSSSLGKTYTCNVDPKPSNTKDKVESKYPGPGSCAPFLGSPSV 241
 DB 61 GLVSLSSVTVPPSSSLGKTYTCNVDPKPSNTKDKVESKYPGPGSCAPFLGSPSV 120
 QY 242 FLPPPKRDTLMTISRTPEVTCVVVDVSOEDPEVQFNMYVDGVEVHNAKTPREEQNSTY 301
 DB 121 FLPPPKRDTLMTISRTPEVTCVVVDVSOEDPEVQFNMYVDGVEVHNAKTPREEQNSTY 180
 QY 302 RVSVSVTLVTLHQMWDINGEKYCKVSNKGLPSSIEKTIISKAKQPREPOVYTLPSQEMTK 361
 DB 181 RVSVSVTLVTLHQMWDINGEKYCKVSNKGLPSSIEKTIISKAKQPREPOVYTLPSQEMTK 240
 QY 362 NOVSLTCLVKGFPYPSDIAVWESNGQPNNTKTPPVLDSDGSEFLYSRLTVDKSRWQEG 421
 DB 241 NOVSLTCLVKGFPYPSDIAVWESNGQPNNTKTPPVLDSDGSEFLYSRLTVDKSRWQEG 300
 QY 422 NVFSCSVMEALHNHYTQKSLSLGK 448
 DB 301 NVFSCSVMEALHNHYTQKSLSLGK 327
 RESULT 2
 GC2_HUMAN STANDARD; PRT; 326 AA.
 AC P01859;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE IG gamma-2 chain C region.
 GN IGHG2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 ON NCBI_TaxID=9606;
 RX SEQUENCE OF 2-326 FROM N.A.
 RA MEDLINE=82197621; PubMed=6804948;
 RA Ellison J.W., Hood L.E.;
 RT "Linkage and sequence homology of two human immunoglobulin gamma
 RT heavy chain constant region genes."
 RL Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988(1982).
 RN [12]
 RP SEQUENCE OF 88-115 FROM N.A.
 RC TISSUE=Fetal liver;
 RX MEDLINE=83001943; PubMed=6811139;
 RA Takahashi N., Ueda S., Obata M., Nikaide T., Nakai S., Honjo T.;
 RT "Structure of a human immunoglobulin gamma genes: implications for
 RT evolution of a gene family."
 RL Cell 29:671-679(1982).
 RN [3]
 RP SEQUENCE OF 99-177 AND 310-326 FROM N.A.
 RC TISSUE=Fetal liver;
 RX MEDLINE=84235992; PubMed=6329676;
 RA Krawinkel U., Rabbitts T.H.;
 RT "Comparison of the hinge-coding segments in human immunoglobulin gamma
 RT heavy chain genes and the linkage of the gamma 2 and gamma 4 subclass
 RT genes.";

RL EMBO J. 1:403-407(1982).
 RN [4]
 RP SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL).
 RX MEDLINE=81007873; PubMed=6774012;
 RA Wang A.-C., Tung E., Pudenberg H.H.;
 RT "The primary structure of a human IgG2 heavy chain: genetic,
 RT evolutionary, and functional implications."
 RL J. Immunol. 125:1048-1054(1980).
 RN [5]
 RP SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN ZIE).
 RX MEDLINE=80001357; PubMed=113060;
 RA Connell G.E., Parr D.M., Hofmann T.;
 RT "The amino acid sequences of the three heavy chain constant region
 RT domains of a human IgG2 myeloma protein."
 RL Can. J. Biochem. 57:758-767(1979).
 RN [6]
 RP SEQUENCE OF 238-275 (ZIE).
 RX MEDLINE=80114419; PubMed=118920;
 RA Hofmann T., Parr D.M.;
 RT "A note of the amino acid sequence of residues 381-391 of human
 RT immunoglobulin gamma chains."
 RL Mol. Immunol. 16:923-925(1979).
 RN [7]
 RP REVISIONS TO 25; 59; 60 AND 264-268 (ZIE).
 RA Hofmann T., Parr D.M.;
 RL Submitted (MAR-1980) to the PIR data bank.
 RN [8]
 RP SEQUENCE OF 1-121 (DOT).
 RX MEDLINE=95255298; PubMed=7737190;
 RA Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;
 RT "Characterization of the two unique human anti-flavon monoclonal
 RT immunoglobulins."
 RL Eur. J. Biochem. 228:886-893(1995).
 RN [9]
 RP DISULFIDE BONDS.
 RX MEDLINE=72033500; PubMed=4940472;
 RA Milestein C., Frangione B.;
 RT "Disulphide bridges of the heavy chain of human immunoglobulin G2."
 RL Biochem. J. 121:217-225(1971).
 RN [10]
 RP DISULFIDE BONDS.
 RX MEDLINE=69064124; PubMed=5782707;
 RA Frangione B., Milestein C., Pink J.R.L.;
 RT "Structural studies of immunoglobulin G."
 RL Nature 221:145-148(1969).
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 CC -----
 CC EMBL; J00230; AAB59393.1; -
 DR PIR; A93906; G2HU.
 DR HSSP; P01857; 1FC1.
 DR Genew; HGNC:5526; IGHG2.
 DR MTM; 147110; -
 DR GO; GO:0005624; C:membrane fraction; NAS.
 DR GO; GO:0003823; F:antigen binding activity; TAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003597; IG-cl.
 DR InterPro; IPR003006; IG_MHC.
 DR Pfam; PF00047; Ig; 3.
 DR SMART; SM00407; Igcl; 2.
 DR PROSITE; PS00835; IG_LIKE; 3.
 DR PROSITE; PS00290; IG_MHC; 2.
 KM Immunoglobulin domain; Immunoglobulin C region.
 FT NON_TER 1 1
 FT DOMAIN 1 98 CH1.
 FT 99 110 HINGE.

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 31, 2003, 10:29:10 ; Search time 38.0918 Seconds
(without alignments)
3034.973 Million cell updates/sec

Title: US-09-917-410-6
Perfect score: 2389

Sequence: 1 QVQLVQSGAEVKKPKSSVKV.....MHEALHNHYTQKSLSLSLGK 448

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 8305255

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Minimum DB seq length: 0
Maximum DB seq length: 2
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Maximum DB seq length: 20000000000

Post-processing:	Minimum Match	0%
	Maximum Match	100%

Listing first 45 summaries

Database :

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1:  sp.archaea:23.*
2:  sp.bacteria:.*
3:  sp.fungi:.*
4:  sp.human:.*
5:  sp.invertebrate:.*
6:  sp.mammal:.*
7:  sp.mlc:.*
8:  sp.organelle:.*
9:  sp.plage:.*
10: sp.plant:.*
11: sp.rodent:.*
12: sp.virus:.*
13: sp.unclassified:.*
14: sp.virus:.*
15: sp.bacteriap:.*
16: sp.archaeap:.*
17:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query	Match	Length	DB	ID	Description
	1	1982.5	83.0	473	4	Q8TC63	Q8TC63	homo sapien
	2	1948	81.5	471	4	Q8TC77	Q8TC77	homo sapien
	3	1896	79.4	521	4	Q8N4Y9	Q8N4Y9	homo sapien
	4	1571	65.8	509	4	Q8NF17	Q8NF17	homo sapien
	5	1538	64.4	473	11	Q9DBL4	Q9DBL4	mus musculus
	6	1535	64.3	463	11	Q99JLC	Q99JLC	mus musculus
	7	1531	64.1	473	11	Q99JL25	Q99JL25	mus musculus
	8	1483.5	62.1	468	11	Q99JL31	Q99JL31	mus musculus
	9	1451	60.7	469	11	Q8K3V9	Q8K3V9	mus musculus
	10	1432.5	60.0	474	11	Q8K3H6	Q8K3H6	mus musculus
	11	1428	59.8	437	11	Q9R1A4	Q9R1A4	mus musculus
	12	1409	59.0	473	11	Q9JL205	Q9JL205	mus musculus
	13	1217	50.9	337	6	Q95M34	Q95M34	equus caball
	14	1139.5	47.7	701	4	Q96P08	Q96P08	homo sapien
	15	901	47.7	614	4	Q96NC6	Q96NC6	homo sapien
	16	842.5	35.3	613	11	Q8VCX7	Q8VCX7	mus musculus

ALIGNMENTS

17	833.5	34.9	278	11	Q8WTX1	Q8WTK1 mus sapien
18	815.5	34.1	613	4	Q9BRU0	Q9BTV0 homo sapien
19	812.5	34.0	500	4	Q9BRU0	Q9BVB9 homo sapien
20	807	33.8	597	4	Q96BB9	Q91WCT1 mus musculu
21	791	33.1	481	11	Q91WT1	Q8WY24 homo sapien
22	787	32.9	497	4	Q8WY24	Q8K172 mus musculu
23	784.5	32.8	482	11	Q8K172	Q8VCV5 mus musculu
24	766	32.1	481	11	Q8VCV5	Q8VCX4 mus musculu
25	762	31.9	489	11	Q8VCX4	Q8K0F2 mus musculu
26	760.5	31.8	488	11	Q8K0F2	Q8K0Z4 mus musculu
27	760.5	31.8	496	4	Q96DK0	Q96DZ0 homo sapien
28	759.5	31.8	480	11	Q8K0Z4	Q8NC16 homo sapien
29	756	31.6	493	4	Q8NCL6	Q91WR1 mus musculu
30	755.5	31.6	488	11	Q91WR1	Q96KF8 homo sapien
31	742.5	31.1	494	4	Q96KF8	Q91WCT3 mus musculu
32	735	30.8	481	11	Q91WT3	Q9BUI0 homo sapien
33	730	30.7	597	4	Q9BUI0	Q9BQJ8 homo sapien
34	734	30.6	597	4	Q9BQJ8	Q91I66 mus musculu
35	727.5	30.5	588	11	Q91I66	Q8WUX4 homo sapien
36	724	30.3	588	4	Q8WUX4	Q96A66 homo sapien
37	724	30.3	618	4	Q96A66	Q96X24 mus musculu
38	722	30.2	487	11	Q96X24	Q96EY0 homo sapien
39	715.5	29.9	613	4	Q96EY0	Q8N5K4 homo sapien
40	712	29.8	499	4	Q8N5K4	Q91Z07 mus musculu
41	696.5	29.2	486	11	Q91Z07	Q91WP5 mus musculu
42	693	29.0	479	11	Q91WP5	Q8VEA0 mus musculu
43	687.5	28.8	480	11	Q8VEA0	Q91XEL mus musculu
44	668	28.0	480	11	Q91XEL	Q91X92 mus musculu
45	658.5	27.6	482	11	Q91X92	

RESULT

	PRELIMINARY:	PRT:	473 AA.
AC	09TC63;		
DT	01-JUN-2002 (TEMBLrel. 21, Created)		
DT	01-JUN-2002 (TEMBLrel. 21, Last sequence update)		
DT	01-MAR-2003 (TEMBLrel. 23, Last annotation update)		
DE	Hypotheical protein.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Kidney;		
RA	Strausberg R.;		
RL	Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; BC025985; AAH25985.1; -		
DR	InterPro; IPR000923; BlueCu.1.		
DR	InterPro; IPR007110; IG_1like.		
DR	InterPro; IPR003006; IG_MHC.		
DR	InterPro; IPR003596; IG_v.		
DR	Pfam; PF00047; IG_4.		
DR	SMART; SM00406; IGv. 1.		
DR	PROSITE; PS00196; COPPER BLUE; 1.		
DR	PROSITE; PS00835; IG_LIKE; 4.		
DR	PROSITE; PS00290; IG_MHC; 3.		
KW	Hypotheical protein.		
QO	SEQUENCE 473 AA; 51966 MW; E29920B09BA369F5 CRC64;		

Query Match	83.0%	Score 182.5	DB 4	Length 473
Best Local Similarity	84.3%	Pred. No. 1.1e-162		
Matches 380	Conservative 24	Mismatches 40	Indels 7	Gaps 4

[illegible]

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Db 86 YSPSLRSRYTMSADMSNSFYLTLDSTVTAADTAIVYCAA---GHLMGFGAHMGQGLV 142
Qy 118 TVSSASTKGPSPVFLPACSRSTSESTALGCLVKDYREPEVTYVNSGALTSVHPFPAY 177
Db 143 SVSPASAKGSPVFLPACSRSTSESTALGCLVDYREPEVTYVNSGALTSVHPFPAY 202
Qy 178 LQSSGLYSLSSVTVFPSSSLGTCTYTCNVDPHKPSNTKYDKRVESKYGPSPCPAPFLG 237
Db 203 LQSSGLYSLSSVTVFPSSSLGTCTYTCNVDPHKPSNTKYDKRVESKYGPSPCPAPFLG 262
Qy 238 GPSVFLPFPKPKDTLMSRTPEVTCVVVDVSDPEVQFMWYDGVENNAKTKPREEQ 297
Db 263 GPSVFLPFPKPKDTLMSRTPEVTCVVVDVSDPEVQFMWYDGVENNAKTKPREEQ 322
Qy 298 NSTYRVSVTLTVLHODMLNGEKYCKVSNKGLPSSIEKTSKAKGQPREOYVTLPPSOE 357
Db 323 NSTYRVSVTLTVLHODMLNGEKYCKVSNKGLPSSIEKTSKAKGQPREOYVTLPPSOE 382
Qy 358 EMTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSR 417
Db 383 EMTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSR 442
Qy 418 WQEGNVFSCSVMEHALHNHTYOKSLSLSLGK 448
Db 443 WQEGNVFSCSVMEHALHNHTYOKSLSLSLGK 473

RESULT 2
Q8TC77 PRELIMINARY; PRT; 471 AA.
AC Q8TC77;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strauberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC024289; AA024289.1; -.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG_4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 2.
KW Hypothetical protein.
SQ SEQUENCE 471 AA; 51791 MW; 388F7F4CF58866DE CRC64;

Query Match 81.5%; Score 1948; DB 4; Length 471;
Best Local Similarity 80.4%; Pred. No. 1e-159;
Matches 370; Conservative 37; Mismatches 33; Indels 20; Gaps 5;
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Db 192 HFPAPLQSSGLYSLSSVTVFPSSSLGTCTYTCNVDPHKPSNTKYDKRVESKYGPSPCPAPFLG 251
Qy 229 SCAPAPFLQSSGLYSLSSVTVFPSSSLGTCTYTCNVDPHKPSNTKYDKRVESKYGPSPCPAPFLG 288
Db 252 PCAPAPFLQSSGLYSLSSVTVFPSSSLGTCTYTCNVDPHKPSNTKYDKRVESKYGPSPCPAPFLG 311
Qy 289 KTKPREEQNSTYRVSVTLTVLHODMLNGEKYCKVSNKGLPSSIEKTSKAKGQPREO 348
Db 312 KTKPREEQNSTYRVSVTLTVLHODMLNGEKYCKVSNKGLPSSIEKTSKAKGQPREO 371
Qy 349 VYTLPPSOEEMTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFFLY 408
Db 372 VYTLPPSOEEMTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFFLY 431
Qy 409 SRLTVDKSRWQEGNVFSCSVMEHALHNHTYOKSLSLSLGK 448
Db 432 SKLTVDKSRWQEGNVFSCSVMEHALHNHTYOKSLSLSLGK 471

RESULT 3
Q8N4Y9 PRELIMINARY; PRT; 521 AA.
AC Q8N4Y9;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells from Tonsils;
RA Strauberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC033178; AA033178.1; -.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003597; IG_C1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG_4.
DR SMART; SM00407; IGV; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 2.
KW Hypothetical protein.
SQ SEQUENCE 521 AA; 57156 MW; 2AC7D22E72D6CAA2 CRC64;

Query Match 79.4%; Score 1896; DB 4; Length 521;
Best Local Similarity 71.9%; Pred. No. 3.7e-155;
Matches 361; Conservative 37; Mismatches 50; Indels 54; Gaps 3;
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 31, 2003, 10:33:16 ; Search time 46,1821 Seconds

(without alignments)
1539.764 Million cell updates/sec

Title: US-09-917-410-6

Perfect score: 2389

Sequence: 1 QVQLVSGAVERKPPGSSVKY.....MHBALNHYTQKSLISLQK 448

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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24: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
25: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	2265.5	94.8	AA28808	pre-5A8 humanised
2	2162.5	90.5	AAW14941	3F4 Human IgG4 exp
3	2162.5	90.5	AAW14938	Murine anti-porcine
4	2159.5	90.4	AAW14935	Humanised 323/A3 (
5	2153.5	90.1	AAW14932	Humanised 323/A3 (
6	2121	88.8	AAW14935	2A2 Human IgG4 exp
7	2121	88.8	AAW14932	Murine anti-porcine
8	2111	88.4	AAW14932	Anti-human IL-4 hu
9	2106.5	88.2	AAW13564	Humanised anti-L-s

10	2101.5	88.0	449	14	AAW43339	Completely humanis
11	2101.5	88.0	449	19	AAW49816	Amino acid sequenc
12	2098.5	87.8	447	18	AAW10232	TF8-5G9 CDR-graft
13	2093.5	87.6	470	21	AAW90936	Humanised HFE7A de
14	2093.5	87.6	470	23	AAW49945	Humanised anti-Fas
15	2093.5	87.6	470	23	AAW74296	Anti-human AIL1m m
16	2086.5	87.3	470	21	AAW90935	Humanised anti-Fas
17	2086.5	87.3	470	21	AAW49904	Mouse humanised an
18	2085.5	87.3	470	21	AAW90934	Humanised anti-Fas
19	2085.5	87.3	470	23	AAW49903	Mouse humanised an
20	2083.5	87.2	470	21	AAW90933	Humanised anti-Fas
21	2083.5	87.2	470	23	AAW49902	Humanised anti-Fas
22	2082.5	87.2	472	23	AAW51695	5G1.1-TPO heavy ch
23	2080.5	87.1	470	19	AAW83037	Anti-Fas humanised
24	2080.5	87.1	470	21	AAW14779	Humanised anti-Fas
25	2080.5	87.1	470	21	AAW90929	Humanised HFE7A de
26	2080.5	87.1	470	23	AAW49898	Humanised anti-Fas
27	2080.5	87.1	470	23	AAW74944	Humanised anti-Fas
28	2079	87.0	448	23	AAW99224	Chimeric CD45RO/RB
29	2077	86.9	583	22	AAW83156	Ganglioside GM2 an
30	2069.5	86.6	652	19	AAW48650	Heavy chain of hMA
31	2069	86.6	463	18	AAW14939	3F4 (Chimeric) hum
32	2069	86.6	463	18	AAW14940	3F4 (Chimeric) hum
33	2067.5	86.5	470	19	AAW83036	Anti-Fas humanised
34	2067.5	86.5	470	21	AAW14776	Humanised anti-Fas
35	2067.5	86.5	470	21	AAW90926	Humanised HFE7A de
36	2067.5	86.5	470	23	AAW49895	Humanised anti-Fas
37	2067.5	86.5	470	23	AAW74941	Humanised anti-Fas
38	2061	86.3	731	22	AAW52156	Humanised HMPG-1 h
39	2061	86.3	741	22	AAW52159	Humanised HMPG-1 h
40	2056	86.1	729	22	AAW52158	Humanised HMPG-1 h
41	2056	86.1	729	22	AAW52161	Humanised HMPG-1 h
42	2053	85.9	730	22	AAW52157	Humanised HMPG-1 h
43	2053	85.9	740	22	AAW52160	Humanised HMPG-1 h
44	2051	85.9	461	22	AAW72236	Humanised 323/A3 (
45	2050.5	85.8	476	24	ABU08022	Monoclonal rabies

ALIGNMENTS

RESULT 1	
AA28808	AA28808 standard; Protein; 468 AA.
ID	AA28808
AC	AA28808;
XX	
DT	25-MAR-2003 (updated)
DT	02-APR-1993 (first entry)
XX	
DE	pre-5A8 humanised heavy chain.
XX	
KW	Vector: PMDR1002; Nocti; HindIII; PMDR1001; pSAB12; pBAC101; E. coli;
KW	UA221(Ig); ampicillin; resistance; immunoglobulin; signal sequence;
KW	humanised; 5A8; heavy chain; variable; region; HV; IgG4; constant;
KW	HC; antibody; homolog; CD4; gp120; cell surface glycoprotein; CD4+;
KW	lymphocytes; helper; inducer; HIV; syncytia; formation.
XX	
OS	Synthetic.
XX	
FT	Key
FT	Peptide
FT	Location/Qualifiers
FT	1..19
FT	/note= "Immunoglobulin signal peptide"
FT	20..141
FT	/note= "Humanised 5A8 HV"
FT	142..468
FT	/note= "Human IgG4 HC"
XX	
PN	WO9209305-A1.
XX	
PD	11-JUN-1992.
XX	
PF	27-NOV-1991; 91WO-US08843.

Query Match	Best Local Similarity	94.8%	Score 2265.5	DB 13	Length 468
Matches 428	Conservative	8	Mismatches 11	Indels 3	Gaps 2
QY	1	QVQLVQSGAEYVKPPSSSVKSVCSKAGYFTFSVVMHVMVROAPQGLGEMTGYTPYNDGTRY	60		
DB	20	QVQLVQSGAEYVKPPSSSVKSVCSKAGYFTFSVVMHVMVROAPQGLGEMTGYTPYNDGTRY	79		
QY	61	NEKFGKRVITTSDESTNTAYMELSGLSRSEDYAVVYCAEEKXGNYV-RYFDVWGQGLTVT	118		
DB	80	DEKFGKRVITTVLDPSTNTAYMELSGLSRSEDYAVVYCAEER-DNYATGAMFAWAGGTLVTV	138		
QY	119	VSSASTKPSVPEPLAPCSRSTSESTALAGCLVKDIFPEPVYVSNWSGALTSVHFFPAVL	178		
DB	139	VSSASTKPSVPEPLAPCSRSTSESTALAGCLVKDIFPEPVYVSNWSGALTSVHFFPAVL	198		
QY	179	QSSGLYSLSSVYTVSSSLGTITTYICNDVHKSNFKVNRVSKYKGPCCSPCAEFLLGG	238		
DB	199	QSSGLYSLSSVYTVSSSLGTITTYICNDVHKSNFKVNRVSKYKGPCCSPCAEFLLGG	258		
QY	239	PSVFLFPPPKPQDITLMISRTPEVTCVVVDVSOEDPEVQFNMYDGVENAHAKTKPREDFN	298		
DB	259	PSVFLFPPPKPQDITLMISRTPEVTCVVVDVSOEDPEVQFNMYDGVENAHAKTKPREDFN	318		
QY	299	STYRVASVLTLYLHQMUNGKEKCKVSNKGLPSSLEKTIISRAKKGPREPOVYTLPPSOE	358		
DB	319	STYRVASVLTLYLHQMUNGKEKCKVSNKGLPSSLEKTIISRAKKGPREPOVYTLPPSOE	378		
QY	359	MTKQVSLTCLVKGFPSPDIAVEMESNGQPENNYKTPPVLDSDSFFLYSLRYDKSRM	418		
DB	379	MTKQVSLTCLVKGFPSPDIAVEMESNGQPENNYKTPPVLDSDSFFLYSLRYDKSRM	438		
QY	419	QEGNVFSCSVNHEALAHNYTKSLSLGK 448			
DB	439	QEGNVFSCSVNHEALAHNYTKSLSLGK 468			

ID	AAW14941	standard: Protein; 464 AA.
XX	AAW14941;	
XX	16-JUN-1997	(first entry)
XX	3F4 Human IgG4 expression plasmid insert product (heavy chain).	
XX	Xenotransplantation; graft rejection; cell interaction; pig;	
XX	vascular cell adhesion molecule; VCAM; monoclonal antibody;	
XX	chimeric antibody; diagnosis.	
XX	Mus sp.	
XX	WO9711971-A1.	
XX	03-APR-1997.	
XX	27-SEP-1996;	96WO-US15575.
XX	26-SEP-1996;	96US-0004489.
XX	28-SEP-1995;	95US-0004489.
XX	(ALEX-) ALEXION PHARM INC.	
XX	Evans MJ, Matlis LA, Mueller EE, Mueller JP, Rollins S;	
XX	Rother RP;	
XX	WPI; 1997-212855/19.	
XX	N-PSDB; AAT62938.	
XX	Antibodies binding to porcine but not human cell interaction	
XX	proteins - useful to treat and assay for rejection of xenografted	
XX	porcine organs, tissues or cells	
XX	Disclosure: Page 62-64; 105pp; English.	
XX	Heavy chain (AAW14941) and light chain (AAW14942) sequences	
XX	correspond to murine anti-porcine soluble vascular cell adhesion	
XX	molecule (VCAM) monoclonal antibody 3F4 (see also AAW14937-38). They	
XX	are encoded by a 3F4 human IgG4 expression plasmid insert (see	
XX	also AAT62938). A chimeric antibody specific for porcine VCAM can be	
XX	produced in transfected host cells. It is useful for diagnosing	
XX	human rejection of porcine xenotransplants and for improving	
XX	xenotransplantation of porcine cells, tissues and organs into human	
XX	recipients.	
XX	Sequence 464 AA;	
XX	Query Match 90.5%; Score 2162.5; DB 18; Length 464;	
XX	Best Local Similarity 90.4%; Pred. No. 1,1e-124;	
XX	Matches 405; Conservative 18; Mismatches 22; Indels 3; Gaps 1	
QY	1 QVQLVQSGAEVKKPGSSSVKVCCKASGYSFTTSYVMHWVRQAPQGLIEWITGIYPYNDGTYK 60	
DB	20 QVQVQSGAEIARPAWASVYKLSCKASGVNFNSYMQVQKRPQGLIEWIGAIYPGDGDISY 79	
QY	61 NEKFKGRYTTISDESTINAYWEISSLREDDTAIVYCCAEVEGNYRYRPDWQCGTLVNY 120	
DB	80 TQFKRGKATLADKSSSTAYMQLSLSLAEDSAVYVCARIVGG--YFDYMQCGTTLTVS 136	
QY	121 SASTGSPVFPPLAPCSRSTSESTALGCLVNDYFPEPTVSNVSGALNSGVTPPAVLQS 180	
DB	137 SASTGSPVFPPLAPCSRSTSESTALGCLVNDYFPEPTVSNVSGALNSGVTPPAVLQS 196	
QY	181 SGLYSLSSVYVPSSSLGCTKYTCNVDDHKPSNTKYVDKVESKYGPCSCPAEFLGPRS 240	
DB	197 SGLYSLSSVYVPSSSLGCTKYTCNVDDHKPSNTKYVDKVESKYGPCSCPAEFLGPRS 256	
QY	241 VFLPFRKDTLMISRTPEVTCCVVVDVSGEDPEVQFNMYVDGCVVHNAKTKRREQFNST 300	

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OM protein - protein search, using sw model

Run on: December 31, 2003, 10:32:16 ; Search time 34.7208 Seconds

(without alignments)
2588.856 Million cell updates/sec

Title: US-09-917-410-6

Perfect score: 2389
Sequence: 1 QVQLVQSGAEVKKRQSSVKV.....MHEALNHYTKSLSLSLGK 448

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 733937 seqs, 200641211 residues

Total number of hits satisfying chosen parameters: 733937

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*
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2: /cgn2_6/ptodata/1/pubppaa/PCT_NEW_PUB.pep:*
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6: /cgn2_6/ptodata/1/pubppaa/PCTUS_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	2226	93.2	467	12	US-10-428-408A-30
3	2115	88.5	465	12	US-10-401-344-2
4	2106.5	88.2	443	9	US-09-917-410-4
5	2093.5	87.6	470	10	US-09-859-053-28
6	2093.5	87.6	470	12	US-10-384-933-157
7	2093.5	87.6	470	15	US-10-384-484-157
8	2086.5	87.3	470	12	US-10-384-933-147
9	2086.5	87.3	470	15	US-10-216-484-147
10	2085.5	87.3	470	12	US-10-384-933-145
11	2085.5	87.3	470	15	US-10-216-484-145
12	2083.5	87.2	470	12	US-10-384-933-143
13	2083.5	87.2	470	15	US-10-216-484-143
14	2082.5	87.2	472	12	US-10-307-724-67
15	2082.5	87.2	472	15	US-10-006-593-67

16	2081	87.1	461	10	US-09-249-011A-24	Sequence 24, Appl
17	2080.5	87.1	470	12	US-10-384-933-117	Sequence 117, App
18	2080.5	87.1	470	15	US-10-216-484-117	Sequence 117, App
19	2067.5	86.5	470	12	US-10-384-933-89	Sequence 89, Appl
20	2067.5	86.5	470	15	US-10-216-484-89	Sequence 89, Appl
21	2061	86.3	731	10	US-09-825-012-46	Sequence 46, Appl
22	2061	86.3	741	10	US-09-825-012-55	Sequence 55, Appl
23	2059	86.2	448	12	US-10-353-708-48	Sequence 48, Appl
24	2059	86.2	448	12	US-10-353-708-60	Sequence 60, Appl
25	2059	86.2	448	15	US-10-171-452A-48	Sequence 48, Appl
26	2059	86.2	448	15	US-10-171-452A-60	Sequence 60, Appl
27	2059	86.2	467	12	US-10-353-708-41	Sequence 41, Appl
28	2059	86.2	467	12	US-10-353-708-47	Sequence 47, Appl
29	2059	86.2	467	12	US-10-353-708-59	Sequence 59, Appl
30	2059	86.2	467	15	US-10-171-452A-41	Sequence 41, Appl
31	2059	86.2	467	15	US-10-171-452A-47	Sequence 47, Appl
32	2059	86.2	467	15	US-10-171-452A-59	Sequence 59, Appl
33	2056	86.1	448	12	US-10-353-708-42	Sequence 42, Appl
34	2056	86.1	448	12	US-10-353-708-54	Sequence 54, Appl
35	2056	86.1	448	15	US-10-171-452A-42	Sequence 42, Appl
36	2056	86.1	448	15	US-10-171-452A-54	Sequence 54, Appl
37	2056	86.1	467	12	US-10-353-708-53	Sequence 53, Appl
38	2056	86.1	467	15	US-10-171-452A-53	Sequence 53, Appl
39	2056	86.1	729	10	US-09-825-012-52	Sequence 52, Appl
40	2056	86.1	729	10	US-09-825-012-61	Sequence 61, Appl
41	2053	85.9	730	10	US-09-825-012-49	Sequence 49, Appl
42	2053	85.9	740	10	US-09-825-012-58	Sequence 58, Appl
43	2050.5	85.8	476	12	US-10-225-108A-16	Sequence 16, Appl
44	2033	85.1	452	11	US-09-726-258-71	Sequence 71, Appl
45	2026.5	84.8	476	10	US-09-747-669-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-09-917-410-6
; Sequence 6, Application US/09917410
; Patent No. US20020098183A1
GENERAL INFORMATION:
APPLICANT: MARTIN, Ulrich; HASSELBECK, Anton; SCHUMACHER, Guenther;
CO, Man S.
TITLE OF INVENTION: ANTI-L-SELECTIN ANTIBODIES FOR PREVENTION OF MULTIPLE ORGAN FAILURE AFTER POLYTRAUMA AND FOR PREVENTION OF ACUTE ORGAN DAMAGE AFTER EXTRACORPOREAL BLOOD CIRCULATION
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Felte & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Computer Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII, WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/917.410
FILING DATE: 26-Jul-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/578,953
FILING DATE: <Unknown>
APPLICATION NUMBER: EP 95 114 969.9
FILING DATE: 19-Sep-95
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, NO. US20020098183A1man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: BOER 1059-BPF/NDH/SLH
TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 688-9200
 TELEFAX: (212) 838-3884
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 448 amino acid residues
 TYPE: amino acid
 TOPOLOGY: linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 6:
 US-09-917-410-6

Query Match 100.0%; Score 2389; DB 9; Length 448;
 Best Local Similarity 100.0%; Pred. No. 8,3e-161;
 Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 QVQLVSGAEVKKPKSSSKVKSCAKSGYFTSYVMHWNRQAPGGGLEWIGYIPYNDGKY 60
DB 1 QVQLVSGAEVKKPKSSSKVKSCAKSGYFTSYVMHWNRQAPGGGLEWIGYIPYNDGKY 60
QY 61 NEKFKGRVITTSDESTNTAYMELSLRSEDTAVYYCAREEYGNVYRFDVWGQGLTVVS 120
DB 61 NEKFKGRVITTSDESTNTAYMELSLRSEDTAVYYCAREEYGNVYRFDVWGQGLTVVS 120
QY 121 SASTKGPSVFPPLAPCSRSTSESTALGCLVKDYFPEPVTVSNWNGALTSGVHTFPAVLQS 180
DB 121 SASTKGPSVFPPLAPCSRSTSESTALGCLVKDYFPEPVTVSNWNGALTSGVHTFPAVLQS 180
QY 121 SASTKGPSVFPPLAPCSRSTSESTALGCLVKDYFPEPVTVSNWNGALTSGVHTFPAVLQS 180
DB 121 SASTKGPSVFPPLAPCSRSTSESTALGCLVKDYFPEPVTVSNWNGALTSGVHTFPAVLQS 180
QY 181 SGLYSLSVTVTPSSSLGKTITTCNVDRKPSNTKVDKRVESKYGPPCSCPAPPEFLGSPS 240
DB 181 SGLYSLSVTVTPSSSLGKTITTCNVDRKPSNTKVDKRVESKYGPPCSCPAPPEFLGSPS 240
QY 181 SGLYSLSVTVTPSSSLGKTITTCNVDRKPSNTKVDKRVESKYGPPCSCPAPPEFLGSPS 240
DB 181 SGLYSLSVTVTPSSSLGKTITTCNVDRKPSNTKVDKRVESKYGPPCSCPAPPEFLGSPS 240
QY 241 VFLEPPKPKDITMISRTPEVTCVVDVDSQEDPEVQFMNYYVDGVEVHNAKTKPREEQFNST 300
DB 241 VFLEPPKPKDITMISRTPEVTCVVDVDSQEDPEVQFMNYYVDGVEVHNAKTKPREEQFNST 300
QY 241 VFLEPPKPKDITMISRTPEVTCVVDVDSQEDPEVQFMNYYVDGVEVHNAKTKPREEQFNST 300
DB 241 VFLEPPKPKDITMISRTPEVTCVVDVDSQEDPEVQFMNYYVDGVEVHNAKTKPREEQFNST 300
QY 301 YRVSVLTVLHODWLNKGEYKCKVSNKGLPSSIIEKTIISKAKGPREPQVYTLPPSQEEMT 360
DB 301 YRVSVLTVLHODWLNKGEYKCKVSNKGLPSSIIEKTIISKAKGPREPQVYTLPPSQEEMT 360
QY 301 YRVSVLTVLHODWLNKGEYKCKVSNKGLPSSIIEKTIISKAKGPREPQVYTLPPSQEEMT 360
DB 301 YRVSVLTVLHODWLNKGEYKCKVSNKGLPSSIIEKTIISKAKGPREPQVYTLPPSQEEMT 360
QY 361 KQVSLTCLVKGFPSPDIAYEWESNGQPENNYKTTTPVLDSDGSFLLYSRLTVDKSRWQE 420
DB 361 KQVSLTCLVKGFPSPDIAYEWESNGQPENNYKTTTPVLDSDGSFLLYSRLTVDKSRWQE 420
QY 421 GNVSFCSVMHEALHNHYTQKSLSLSGK 448
DB 421 GNVSFCSVMHEALHNHYTQKSLSLSGK 448

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RESULT 2 US-10-428-408A-30

Sequence 30, Application US/10428408A
 Publication No. US20030235869A1
 GENERAL INFORMATION:
 APPLICANT: Celltech R&D Limited
 TITLE OF INVENTION: BIOLOGICAL PRODUCTS
 FILE REFERENCE: CARP0004-100
 CURRENT APPLICATION NUMBER: US/10/428,408A
 CURRENT FILING DATE: 2003-05-02
 NUMBER OF SEQ ID NOS: 51
 SOFTWARE: SeqMin99, version 1.02
 SEQ ID NO 30
 LENGTH: 467
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 NAME/KEY: CHAIN
 OTHER INFORMATION: Full sequence of grafted heavy chain
 US-10-428-408A-30

Query Match 93.2%; Score 2226; DB 12; Length 467;
 Best Local Similarity 93.5%; Pred. No. 2,9e-149;
 Matches 419; Conservative 10; Mismatches 19; Indels 0; Gaps 0;

QY 1 QVQLVSGAEVKKPKSSSKVKSCAKSGYFTSYVMHWNRQAPGGGLEWIGYIPYNDGKY 60

```

DB 20 EQLVDSGAEVKKPKGASVVKSCAKSGYFTSNYIHWNRQAPGGGLEWIGINGNVATY 79
QY 61 NEKFKGRVITTSDESTNTAYMELSLRSEDTAVYYCAREEYGNVYRFDVWGQGLTVVS 120
DB 80 RRFQGRVITTSDESTNTAYMELSLRSEDTAVYYCAREEYGNVYRFDVWGQGLTVVS 129
QY 121 SASTKGPSVFPPLAPCSRSTSESTALGCLVKDYFPEPVTVSNWNGALTSGVHTFPAVLQS 180
DB 140 SASTKGPSVFPPLAPCSRSTSESTALGCLVKDYFPEPVTVSNWNGALTSGVHTFPAVLQS 199
QY 181 SGLYSLSVTVTPSSSLGKTITTCNVDRKPSNTKVDKRVESKYGPPCSCPAPPEFLGSPS 240
DB 200 SGLYSLSVTVTPSSSLGKTITTCNVDRKPSNTKVDKRVESKYGPPCSCPAPPEFLGSPS 259
QY 241 VFLEPPKPKDITMISRTPEVTCVVDVDSQEDPEVQFMNYYVDGVEVHNAKTKPREEQFNST 300
DB 260 VFLEPPKPKDITMISRTPEVTCVVDVDSQEDPEVQFMNYYVDGVEVHNAKTKPREEQFNST 319
QY 301 YRVSVLTVLHODWLNKGEYKCKVSNKGLPSSIIEKTIISKAKGPREPQVYTLPPSQEEMT 360
DB 320 YRVSVLTVLHODWLNKGEYKCKVSNKGLPSSIIEKTIISKAKGPREPQVYTLPPSQEEMT 379
QY 361 KQVSLTCLVKGFPSPDIAYEWESNGQPENNYKTTTPVLDSDGSFLLYSRLTVDKSRWQE 420
DB 380 KQVSLTCLVKGFPSPDIAYEWESNGQPENNYKTTTPVLDSDGSFLLYSRLTVDKSRWQE 439
QY 421 GNVSFCSVMHEALHNHYTQKSLSLSGK 448
DB 440 GNVSFCSVMHEALHNHYTQKSLSLSGK 467

```

RESULT 3 US-10-401-344-2

Sequence 2, Application US/10401344
 Publication No. US20030194404A1
 GENERAL INFORMATION:
 APPLICANT: Schering Corporation and Abgenix, Inc.
 APPLICANT: Corvallis, Jose
 TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO INTERLEUKIN-5 AND METHODS AND CO
 FILE REFERENCE: L101564W1
 CURRENT APPLICATION NUMBER: US/10/401,344
 CURRENT FILING DATE: 2003-03-27
 NUMBER OF SEQ ID NOS: 22
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 2
 LENGTH: 465
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: SIGNAL
 LOCATION: (1)..(19)
 OTHER INFORMATION:
 FEATURE:
 NAME/KEY: Variable Region
 LOCATION: (20)..(138)
 OTHER INFORMATION:
 FEATURE:
 NAME/KEY: CH1 Region
 LOCATION: (139)..(236)
 OTHER INFORMATION:
 FEATURE:
 NAME/KEY: Hinge Region
 LOCATION: (237)..(248)
 OTHER INFORMATION:
 FEATURE:
 NAME/KEY: CH2 Region
 LOCATION: (249)..(358)
 OTHER INFORMATION:
 FEATURE:
 NAME/KEY: CH3 Region

FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/578,953
FILING DATE: 27-Dec-95
APPLICATION NUMBER: EP 95 112 895.8
FILING DATE: 17-Aug-95
APPLICATION NUMBER: EP 95 114 969.9
FILING DATE: 19-Sep-95
ATTORNEY/AGENT INFORMATION:
NAME: Norman D. Hanson
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: BOER 1059-PCT-PFF/NDH
TELEPHONE: (212) 688-9200
TELEFAX: (212) 688-3884
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 443
TYPE: amino acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-13152-4

Query Match 88.2%; Score 2106.5; DB 5; Length 443;
Best Local Similarity 88.4%; Pred. No. 1.9e-161;
Matches 396; Conservative 21; Mismatches 26; Indels 5; Gaps 2;

1 QVQLVDSGAEVKKPGSSVKVCKASGYTFSTSYVMHWROAPGQGLEWIGYIYPNDQTKY 60
1 EVQLVESGGGLVQPGSSLRSLCAASGFTFTYAMSWVRQAPGKLEWVASI-STGSGTYY 59
61 NEKFKGRVITTSDESTNTAYMELSLRSEDTAVYYCAREEYGNVRYFDWGGGTLVTVS 120
60 PDSVKGRTISRDNAKNTLYLQNMSLAEPTAVYYCARD---YDGFVDWGGGTLVTVS 115
121 SASTKGPSVPLAPCSRSTSESTALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 180
116 SASTKGPSVPLAPCSRSTSESTALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 175
181 SGLYSLSVTVVSSSLGTQTYTCNVNDRKPSNTKVDKRVESKYPPEPSCPAPPEFLG 240
176 SGLYSLSVTVVSSSLGTQTYTCNVNDRKPSNTKVDKRVESKYPPEPSCPAPPEFLG 235
241 VFLEPPKPKDTLMISRTPEVTCVVDVDSQEDPEVQFMWYDGEVHNAAKTKPREEQF 300
236 VFLEPPKPKDTLMISRTPEVTCVVDVDSQEDPEVQFMWYDGEVHNAAKTKPREEQF 295
301 YRVSVLTVLHODWLNKEKCYKSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMT 360
296 YRVSVLTVLHODWLNKEKCYKSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMT 355
361 KNOVSLTCLVKGFPSDIAVEWESNGQPENNYKTTTPVLDSDGSFLYSRLTYDKSR 420
356 KNOVSLTCLVKGFPSDIAVEWESNGQPENNYKTTTPVLDSDGSFLYSRLTYDKSR 415
421 GNVFSCSVMEHALHNHYTKSLSLGK 448
416 GNVFSCSVMEHALHNHYTKSLSLGK 443

RESULT 4
US-08-458-516-13
Sequence 13, Application US/08458516
Patent No. 577085
GENERAL INFORMATION:
APPLICANT: Co, Man Sung
APPLICANT: Tso, J. Yun
TITLE OF INVENTION: Humanized Antibodies Reactive with
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:

ADDRESSEE: William M. Smith
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,516
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/059,159
FILING DATE: 03-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-37-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 449 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-458-516-13

Query Match 88.0%; Score 2101.5; DB 1; Length 449;
Best Local Similarity 88.7%; Pred. No. 4.9e-161;
Matches 400; Conservative 20; Mismatches 26; Indels 5; Gaps 3;

1 QVQLVDSGAEVKKPGSSVKVCKASGYTFSTSYVMHWROAPGQGLEWIGYIYPNDQTKY 60
1 QVQLVDSGAEVKKPGSSVKVCKASGYTFSTSYVMHWROAPGQGLEWIGYIYPNDQTKY 60
61 NEKFKGRVITTSDESTNTAYMELSLRSEDTAVYYCAREEYGNVRYFDWGGGTLVTVS 120
61 NEKFKGRVITTSDESTNTAYMELSLRSEDTAVYYCAREEYGNVRYFDWGGGTLVTVS 120
121 SASTKGPSVPLAPCSRSTSESTALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 180
119 SASTKGPSVPLAPCSRSTSESTALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 178
181 SGLYSLSVTVVSSSLGTQTYTCNVNDRKPSNTKVDKRVESK---YGPPEPSCPAPPEFLG 237
179 SGLYSLSVTVVSSSLGTQTYTCNVNDRKPSNTKVDKRVESK---YGPPEPSCPAPPEFLG 238
238 GSPVFLPEPPKPKDTLMISRTPEVTCVVDVDSQEDPEVQFMWYDGEVHNAAKTKPREEQF 297
239 GSPVFLPEPPKPKDTLMISRTPEVTCVVDVDSQEDPEVQFMWYDGEVHNAAKTKPREEQF 298
298 NSTYRVSVLTVLHODWLNKEKCYKSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMT 357
299 NSTYRVSVLTVLHODWLNKEKCYKSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMT 358
358 EMTKNOVSLTCLVKGFPSDIAVEWESNGQPENNYKTTTPVLDSDGSFLYSRLTYDKSR 417
359 EMTKNOVSLTCLVKGFPSDIAVEWESNGQPENNYKTTTPVLDSDGSFLYSRLTYDKSR 418
418 WQGNVFSCSVMEHALHNHYTKSLSLGK 448
419 WQGNVFSCSVMEHALHNHYTKSLSLGK 449

RESULT 5
US-09-027-449-71

Sequence 71, Application US/09027449
Patent No. 6025158
GENERAL INFORMATION:
APPLICANT: Gonzalez, Tania R.
APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/027,449
FILING DATE: 20-Feb-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/074,330
FILING DATE: 22-Jan-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/038,664
FILING DATE: 21-Feb-1997
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085R3-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 452 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-027-449-71

Query Match 85.1%; Score 2033; DB 3; Length 452;
Best Local Similarity 84.1%; Pred. No. 1.6e-155;
Matches 382; Conservative 33; Mismatches 31; Indels 8; Gaps 3;

QY 1 QVQLVQSGAEVKKPKSSVKVSCKASGYTFTSYVMHWVRQAPGQGLEWIGYIYPNDGTY 60
DB 1 EVQLVQSGGGLVQPGGSLRLSCAASGYFSFSHYMHVVRQAPGKGLIEWGYIDPSNGETTY 60
QY 61 NEKFKGRVTITSDSTNTAYMELSLRSEDYAVYYCAREEY---GNYRYFEDVMQGLTY 117
DB 61 NQKFKGRFTLSRDNSKNTAYLQMNSLRAEDYAVYYCARDDYRNGDM--FEDVMQGLTY 118
QY 118 TVSSASTGSPVFPPLAPCSRSTSESTAAAGCLVQDYFPEPTVSNMNSGALTSGVHTFPAY 177
DB 119 TVSSASTGSPVFPPLAPSKSTSGGTAALGCLVKDYFPEPTVSNMNSGALTSGVHTFPAY 178
QY 178 LQSSGLYSLSSVYTPSSSLGTYTTCNVNDRKPSNTKVDKRVESK---YGPSPCPSPAPE 234
DB 179 LQSSGLYSLSSVYTPVSSSLGTYTTCNVNDRKPSNTKVDKRVESKCDTHCPCPAPE 238
QY 235 FLGGPSVFLPPPKPKDTLMISRTPEYTCVVVDVSDPEVQFNWYVDGVEVHNAKTKPRE 294
DB 239 LLGGPSVFLPPPKPKDTLMISRTPEYTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 298
QY 295 EQPNSTYRVVSVLTVLDHOMLNGKEYKCVVSNKGLPSSIEKTIKSKAKGQPREPQVYTLPP 354
DB 299 EQNSTYRVVSVLTVLDHOMLNGKEYKCVVSNKGLPSEKTIKSKAKGQPREPQVYTLPP 358

QY 355 SQEEMTNQVSLTCLVKGFIYPSDIAVWESNGPENNYKTTTPVLDSDGSFLLYSRLTVD 414
DB 359 SREEMTNQVSLTCLVKGFIYPSDIAVWESNGPENNYKTTTPVLDSDGSFLLYSRLTVD 418
QY 415 KSRWQGNVFSQSVMEALNHNHYTKSLSLGK 448
DB 419 KSRWQGNVFSQSVMEALNHNHYTKSLSLSPK 452

RESULT 6

US-09-026-985-71
Sequence 71, Application US/09026985
Patent No. 6133426

GENERAL INFORMATION:
APPLICANT: Gonzalez, Tania R.
APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/026,985
FILING DATE: 20-Feb-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085R3-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 452 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-026-985-71

Query Match 85.1%; Score 2033; DB 3; Length 452;
Best Local Similarity 84.1%; Pred. No. 1.6e-155;
Matches 382; Conservative 33; Mismatches 31; Indels 8; Gaps 3;

QY 1 QVQLVQSGAEVKKPKSSVKVSCKASGYTFTSYVMHWVRQAPGQGLEWIGYIYPNDGTY 60
DB 1 EVQLVQSGGGLVQPGGSLRLSCAASGYFSFSHYMHVVRQAPGKGLIEWGYIDPSNGETTY 60
QY 61 NEKFKGRVTITSDSTNTAYMELSLRSEDYAVYYCAREEY---GNYRYFEDVMQGLTY 117
DB 61 NQKFKGRFTLSRDNSKNTAYLQMNSLRAEDYAVYYCARDDYRNGDM--FEDVMQGLTY 118
QY 118 TVSSASTGSPVFPPLAPCSRSTSESTAAAGCLVQDYFPEPTVSNMNSGALTSGVHTFPAY 177
DB 119 TVSSASTGSPVFPPLAPSKSTSGGTAALGCLVKDYFPEPTVSNMNSGALTSGVHTFPAY 178
QY 178 LQSSGLYSLSSVYTPSSSLGTYTTCNVNDRKPSNTKVDKRVESK---YGPSPCPSPAPE 234
DB 179 LQSSGLYSLSSVYTPVSSSLGTYTTCNVNDRKPSNTKVDKRVESKCDTHCPCPAPE 238
QY 235 FLGGPSVFLPPPKPKDTLMISRTPEYTCVVVDVSDPEVQFNWYVDGVEVHNAKTKPRE 294
DB 239 LLGGPSVFLPPPKPKDTLMISRTPEYTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 298

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QY      295 EGNSTAYRVSVLTTLVHQMUNGKCKCYNKG.PSISIEKTIISAAGQPREPOVTLTP 35
       |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::| 36
Db      299 EQNSTIRYVSULTLVHQMUNGKCKCYNKALPAPEKTIISAAGQPREPOVTLTP 350
QY      355 SOEEMTKNOVSLTCLVKGFYPSPDIAMWESNQPENNYKTTPVLDSGSPFLYSRLTVD 414
       |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::| 415
Db      415 KSRMOEGNVFSCVMHEALHNHYTOKSLISLIGK 448
       |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::| 449
       419 KSRMOCQGVNFSCVMHEALHNHYTOKSLISLSPGK 452
       |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::| 453

RESULT 7
US-09-121-952A-71
Sequence 71, Application US/09121952A
Patent No. 6458355
GENERAL INFORMATION:
APPLICANT: Genentech, Inc., Hseil, Vanessa
APPLICANT: Kouments, Iphigenia
APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
APPLICANT: Shahrokhi, Zahra
TITLE OF INVENTION: METHODS OF TREATING INFLAMMATORY DISEASES
TITLE OF INVENTION: WITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER CONJUGATES
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 Inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/121,952A
FILING DATE: 24-Jul-1998
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/074330
FILING DATE: 22-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/075467
FILING DATE: 20-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085R4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 452 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear

```

	Query March	85.1%	Score 2033;	DB 4	length 452;
	Best Local Similarity	84.1%	Pred. No. 1,6e-155;		
	Matches 382;	Conservative 33;	Mismatches 31;	Indels 8;	Gaps 3
OY	1 OVOLVQSGAAEVKKRPSSTXYKVCCKAGCAFTPTSYVMHMMWQAOPAQGLGEMNGIYIPYPNDGRKY				60
	:::::	:	:	:	
Dd	1 EVQLVDSGGGLVAPPGSIFRLSCAASGAEYSSTSSIMFMHWRAQPAFGKGLSEMGVIDPDSNGETTY				60
OY	61 NEKEFGRVTITSDSENTINAYNELSLREEDTAIVYYCAEEY--GNVYRFEDVWGQGTLY				117

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Db      61 NQXFKRFLTSDNSKNTAYILOMNSLRBEDTAYVYCARGDVRNNGDM--FFDWGOGTLV 118
QY      118 TVSSASTKPSVFPPLAPCSRSTSESTAALGCLVNDPEPEPVYWSNGALTSGVHTPEAV 177
      119 TVSSASTKPSVFPPLAPSKSTSGTALGCLVNDFFPEPVYWSNGALTSGVHTPEAV 178
QY      178 LQSSGLYSLSVVYWPSSLSGTXYTCNVDPKPSNTKYDKRVEK--YGDPCSPCAPE 234
      179 LQSSGLYSLSVVYWPSSLSGTQTYICNVNHPKSNTRYDKKVEPKSCDKHTTCCPCAPE 238
QY      235 FLGGBSVFLPFPKPKDTLMIKSTBEVTCVYVDVSOEDPEVQPNMYVYDGVETHNAKTPRE 294
      239 LFGSPVFLFPKPKDTLMIKSTBEVTCVYVDVSHEDPEVQPNMYVYDGVETHNAKTPRE 298
QY      295 EQNNSYRVRVSVLTVLHDQMLNGKREYKCKVSNKGLPSSIEXTIKSAQOPREPOVYTLPP 354
      299 EQNNSYRVRVSVLTVLHDQMLNGKREYKCKVSNKGLPAIEIKTISKAQOPREPOVYTLPP 358
QY      355 SQEEMTKNOVSLTCLYKGFYPSDIAVEMESNGQPENNYKTPPVLJDSGSPFLYSRLTVD 414
      359 SREEMTKNOVSLTCLYKGFYPSDIAVEMESNGQPENNYKTPPVLJDSGSPFLYSRLTVD 418
Db      415 KSRWQGNVFCSCVMEALHNHYTKSLSLSLGK 448
      419 KSRWQGNVFCSCVMEALHNHYTKSLSLSLPGK 452

```

RESULT 8
US-09-234-340A-71
: Sequence 71. Application US/09234340A
: Patent No. 6468532
: GENERAL INFORMATION:
: APPLICANT: Genentech, Inc., Hseil, Vanessa
: APPLICANT: Koumentsis, Iphigenia
: APPLICANT: Leong, Steven R.
: APPLICANT: Presta, Leonard G.
: APPLICANT: Shahrokh, Zahra
: APPLICANT: Zapata, Gerardo A.
: TITLE OF INVENTION: METHODS OF TREATING INFLAMMATORY DISEASES
: TITLE OF INVENTION: WITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER CONJUGATES
: NUMBER OF SEQUENCES: 72
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genentech, Inc.
: STREET: 1 DNA Way
: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: WinPacIn (Genentech)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/234,340A
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/09/121,952
: FILING DATE: 24-Jul-1998
: APPLICATION NUMBER: 60/074330
: FILING DATE: 22-JAN-1998
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 60/075467
: FILING DATE: 20-FEB-1998
: ATTORNEY/AGENT INFORMATION:
: NAME: Love, Richard B.
: REGISTRATION NUMBER: 34,659
: REFERENCE/DOCKET NUMBER: P105R4
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 650/225-5530
: TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 452 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-234-340A-71

Query Match 85.1%; Score 2033; DB 4; Length 452;
Best Local Similarity 84.1%; Pred. No. 1.6e-155;
Matches 382; Conservative 33; Mismatches 31; Indels 8; Gaps 3;

```
OY 1 QVQLVQSGAEVKKPKSSSKAKVCKASGCTFTSYVMHWVRQAPGQGLEWIGYIPYNDGK 60
DB 1 EVQLVQSGGGLVQPGSGLRLSCAASGYSFSSHYMHVQAQPGKLEWVGYPDPSGGETTY 60
OY 61 NEKFKGRVTITSDSTNTAYMELSLRSEDYAVYCARREYVYFVWVGQGLTV 117
DB 61 NQKFKGRFTLSRDNSKNTAIYLOMNSLRADDTAVYICAGDGRYNDG--FDVWVGQGLTV 118
OY 118 TVSSASTKGPVFPPLAPCSRSTSESTAALGCLVKDYFPEPVTVSNMGSALTSGVHTFPAV 177
DB 119 TVSSASTKGPVFPPLAPSKSTSGTAAIGCLVKDYFPEPVTVSNMGSALTSGVHTFPAV 178
OY 178 LOSSELVSLSSVTVTPSSSLGRTKTTTCNVDRHPSNTKYDKVRSK---YGPCCPCPAPE 234
DB 179 LOSSELVSLSSVTVTPSSSLGRTQTYICNVNRHPSNTKYDKVPEPSCDKTHTCPCPAPE 238
OY 235 FLGGSVFLFPKPKDITMISRTPEVTCVVDVDSQEDPEVQFMWYVDGEVHNAKTPRE 294
DB 239 ILGGSVFLFPKPKDITMISRTPEVTCVVDVSHEDPEVKRWYVDGEVHNAKTPRE 298
OY 295 EQFNSTYRVSVLTVAHQDMLNGEKYCKVSNKGLPSSIEKTISSAKGQPREPQVYTLPP 354
DB 299 EQFNSTYRVSVLTVAHQDMLNGEKYCKVSNKGLPAPIEKTISSAKGQPREPQVYTLPP 358
OY 355 SEENTKQVSLTCLVKGFPSPDIAYEWESNGQPENNYKTPPVLDSDGSFPLYSLRYVD 414
DB 359 SEENTKQVSLTCLVKGFPSPDIAYEWESNGQPENNYKTPPVLDSDGSFPLYSLRYVD 418
OY 415 KSRMOEGNVFSCSVMEALHNHYTOKSLSLSGK 448
DB 419 KSRMOEGNVFSCSVMEALHNHYTOKSLSLSPGK 452
```

RESULT 9
US-08-523-894-8
Sequence 8, Application US/08523894
Patent No. 6136310

GENERAL INFORMATION:
APPLICANT: Hanna, Nabil
APPLICANT: Newman, Roland A.
APPLICANT: Reff, Mitchell E.
TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
TITLE OF INVENTION: Therapy
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314-3187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/523,894
FILING DATE: 06-SEP-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.

REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-165
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-523-894-8

Query Match 84.8%; Score 2026; DB 3; Length 467;
Best Local Similarity 85.5%; Pred. No. 6.1e-155;
Matches 384; Conservative 19; Mismatches 44; Indels 2; Gaps 2;

```
OY 1 QVQLVQSGAEVKKRQSSKAKVCKASGCTFTSYVMHWVRQAPGQGLEWIGYIPYNDGK 59
DB 20 QVQLVQSGPGVLPKSEETSLTCSVSGSISGDYFWIRQSPGKLEWIGIYVSGGGIN 79
OY 60 YNEKFKGRVTITSDSTNTAYMELSLRSEDYAVYCARREYVYFVWVGQGLTV 119
DB 80 YNPGLNRRVTSISDTSKLPFLKRSVTAADTAAYCA-SMLKYLHMLTWGQGLTV 138
OY 120 SSASTKGPVFPPLAPCSRSTSESTAALGCLVKDYFPEPVTVSNMGSALTSGVHTFPAV 179
DB 139 SSASTKGPVFPPLAPCSRSTSESTAALGCLVKDYFPEPVTVSNMGSALTSGVHTFPAV 198
OY 180 SSGVLSLSSVTVTPSSSLGRTKTTTCNVDRHPSNTKYDKRVSKYGPCCPCPAPEFLG 239
DB 199 SSGVLSLSSVTVTPSSSLGRTQTYICNVDRHPSNTKYDKRVSKYGPCCPCPAPEFLG 258
OY 240 SVFLFPKPKDITMISRTPEVTCVVDVDSQEDPEVQFMWYVDGEVHNAKTPREEQNS 299
DB 259 SVFLFPKPKDITMISRTPEVTCVVDVDSQEDPEVQFMWYVDGEVHNAKTPREEQNS 318
OY 300 TYRVSVLTVAHQDMLNGEKYCKVSNKGLPSSIEKTISSAKGQPREPQVYTLPPSQEEM 359
DB 319 TYRVSVLTVAHQDMLNGEKYCKVSNKGLPSSIEKTISSAKGQPREPQVYTLPPSQEEM 378
OY 360 TKQVSLTCLVKGFPSPDIAYEWESNGQPENNYKTPPVLDSDGSFPLYSLRYVDKSNQ 419
DB 379 TKQVSLTCLVKGFPSPDIAYEWESNGQPENNYKTPPVLDSDGSFPLYSLRYVDKSNQ 438
OY 420 EGNVFCSCVMHEALHNHYTOKSLSLSGK 448
DB 439 EGNVFCSCVMHEALHNHYTOKSLSLSGK 467
```

RESULT 10
US-09-301-593-43
Sequence 43, Application US/09301593A
Patent No. 6455677

GENERAL INFORMATION:
APPLICANT: Park, John E.
APPLICANT: Garin-Chesa, Pilar
APPLICANT: Bamberger, Uwe
APPLICANT: Leger, Olivier
APPLICANT: Saldanha, Jose W.
APPLICANT: Retig, Wolfgang J.
TITLE OF INVENTION: FAP-specific Antibody with Improved Productivity
FILE REFERENCE: 0652.1890001
CURRENT APPLICATION NUMBER: US/09/301,593A
CURRENT FILING DATE: 1999-04-29
EARLIER APPLICATION NUMBER: EP 98107925.4
EARLIER FILING DATE: 1998-04-30
EARLIER APPLICATION NUMBER: US 60/086,049
EARLIER FILING DATE: 1998-05-18
NUMBER OF SEQ ID NOS: 108
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 43
LENGTH: 472

TYPE: PRT
ORGANISM: Homo sapiens
US-09-301-593-43

Query Match 84.7%; Score 2023.5; DB 4; Length 472;
Best Local Similarity 86.1%; Pred. No. 9.8e-155;
Matches 391; Conservative 17; Mismatches 39; Indels 7; Gaps 4;

QY 1 QVQVVGAGVKKRGSSVVKSCAKAGYFTSYVMHWRAQDQGLEWIGYIYPNDGTY 60
DB 20 QVQVVGAGVKKRGSSVVKSCAKAGYFTSYVMHWRAQDQGLEWIGYIYPNDGTY 79
QY 61 NEKRGRTITSDSTNTAYMELSLRSEDYAVYCAEE--YGVNRYRDWVGQGLV 117
DB 80 NQKRGRTITVGASASTAYMELSLRSEDYAVYCAEIRIAYGDEGHANDYVGQGLV 139
QY 118 TVSSASTKGPVFLAPCSRSTSESTALGCLVVDYFPEPYTVSMNSGALTSYHTFPAY 177
DB 140 TVSS-STKGPVFLAPCSRSTSGGTALGCLVVDYFPEPYTVSMNSGALTSYHTFPAY 198
QY 178 LQSSGLVSLSSVTVPPSSSLGTQTYTCNVDHKPSNTKYDKRVEK--YGPCCPSCPAE 234
DB 199 LQSSGLVSLSSVTVPPSSSLGTQTYTCNVNHKPSNTKYDKRVEKSCDKHTCCPCPAE 258
QY 235 FLGSPVFLPPPKKDTLMISRTEVTCVVVDVSGQEDPEVQFNMYVDGVEVHNAKTKPRE 294
DB 259 LLGGPSVFLPPPKKDTLMISRTEVTCVVVDVSHEDPEVQFNMYVDGVEVHNAKTKPRE 318
QY 295 EQFSTRYRVSVLTVLHODMLNGEKYCKVSNKGLPSIETIKISKAGQPREPOVYTLPP 354
DB 319 EQVNSTRYRVSVLTVLHODMLNGEKYCKVSNKGLPSIETIKISKAGQPREPOVYTLPP 378
QY 355 SQEEMTKNQVSLTCLVKGFPYSDIAVEMESNGQEPNNYKTPPYLDSDGSFFLYSRLTVD 414
DB 379 SREMTKNQVSLTCLVKGFPYSDIAVEMESNGQEPNNYKTPPYLDSDGSFFLYSRLTVD 438
QY 415 KSRWQEGNVFSCSYMHGALHNHYTKSLSLGK 448
DB 439 KSRWQEGNVFSCSYMHGALHNHYTKSLSLSPGK 472

RESULT 11

US-08-378-939-10
Sequence 10, Application US/08378939
Patent No. 5876961
GENERAL INFORMATION:
APPLICANT: CROME, JAMES SCOTT
APPLICANT: LEWIS, ALAN PETER
TITLE OF INVENTION: PRODUCTION OF ANTIBODIES
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ
STREET: 555 THIRTEENTH ST. N.W.
CITY: WASHINGTON
STATE: D. C.
COUNTRY: U.S.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,939
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/952640
FILING DATE: 01-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: ERNST, BARBARA G
REGISTRATION NUMBER: 30,377
REFERENCE/DOCKET NUMBER: 1808-118

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 783-6040
TELEFAX: (202) 783-6031
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 476 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-378-939-10

Query Match 84.7%; Score 2023.5; DB 2; Length 476;
Best Local Similarity 84.5%; Pred. No. 9.9e-155;
Matches 386; Conservative 29; Mismatches 33; Indels 9; Gaps 3;

QY 1 QVQVVGAGVKKRGSSVVKSCAKAGYFTSYVMHWRAQDQGLEWIGYIYPNDGTY 60
DB 20 QVQVVGAGVKKRGSSVVKSCAKAGYFTSYVMHWRAQDQGLEWIGYIYPNDGTY 79
QY 61 NEKRGRTITSDSTNTAYMELSLRSEDYAVYCAEE--YGVNRYRDWVGQGLV 114
DB 80 NQKRGRTITADKSTAHMELSLRSEDYAVYCATDRYRQANFDRARVGMFDPWGQGLV 139
QY 115 TVVTSASTKGPVFLAPCSRSTSESTALGCLVVDYFPEPYTVSMNSGALTSYHTFPAY 174
DB 140 TVVTSASTKGPVFLAPCSRSTSGGTALGCLVVDYFPEPYTVSMNSGALTSYHTFPAY 199
QY 175 PAVLQSSGLVSLSSVTVPPSSSLGTQTYTCNVDHKPSNTKYDKRVEK--YGPCCPSCP 231
DB 200 PAVLQSSGLVSLSSVTVPPSSSLGTQTYTCNVNHKPSNTKYDKRVEKSCDKHTCCPCP 259
QY 232 APEFLGSPVFLPPPKKDTLMISRTEVTCVVVDVSGQEDPEVQFNMYVDGVEVHNAKTK 291
DB 260 APEFLGSPVFLPPPKKDTLMISRTEVTCVVVDVSHEDPEVQFNMYVDGVEVHNAKTK 319
QY 292 PREQFSTRYRVSVLTVLHODMLNGEKYCKVSNKGLPSIETIKISKAGQPREPOVYTLPP 351
DB 320 PREQVNSTRYRVSVLTVLHODMLNGEKYCKVSNKGLPSIETIKISKAGQPREPOVYTLPP 379
QY 352 LPPSOEMTKNQVSLTCLVKGFPYSDIAVEMESNGQEPNNYKTPPYLDSDGSFFLYSRLTVD 411
DB 380 LPPSRDELTKNQVSLTCLVKGFPYSDIAVEMESNGQEPNNYKTPPYLDSDGSFFLYSRLTVD 439
QY 412 TVDKSRWQEGNVFSCSYMHGALHNHYTKSLSLGK 448
DB 440 TVDKSRWQEGNVFSCSYMHGALHNHYTKSLSLSPGK 476

RESULT 12

US-08-788-800-12
Sequence 12, Application US/08788800
Patent No. 5914112
GENERAL INFORMATION:
APPLICANT: Bednar, Martin M.
APPLICANT: Thomas, G. Roger
TITLE OF INVENTION: ANTI-CD18 ANTIBODIES IN STROKE
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Minipatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/788,800
FILING DATE: 22-Jan-1997

```
/ CLASSIFICATION: 424
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Lee, Wendy M.
/ REGISTRATION NUMBER: 40,378
/ REFERENCE/DOCKET NUMBER: P0987r1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415/225-1994
/ TELEFAX: 415/952-9881
/ TELEX: 910/371-7168
/ INFORMATION FOR SEQ ID NO: 12:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 450 amino acids
/ TYPE: Amino Acid
/ TOPOLOGY: Linear
/
US-08-788-800-12

Query Match      84.6%; Score 2022; DB 2; Length 450;
Best Local Similarity 84.0%; Pred. No. 1.2e-154;
Matches 379; Conservative 31; Mismatches 37; Indels 4; Gaps 2;

QY 1 QVQLVQSGAEVKKPQSSVKVCASGYSFTSYVMHWRAQPGQGLEWIGYIYPNDGTY 60
DB 1 EVQLVESGGGLVQPGSRLSRATSGYTFETWMHMQAPGKLEWVAGINPKNGTSH 60
QY 61 NEKFKGRTITSDSTNTAYMELSLRSEDTAVYYCAR--EEYGNVYRFYDVGQGTLY 117
DB 61 NORFMDRFTISVDKSTSTAYMQMNSLRADFAVYYCARMKGALNGFDVRFYDVGQGTLY 120
QY 118 TVSSASTGSPVFLAPCSRSTSESTALGCLVKDYFPEPVVSWNSGALTSGVHTFPAV 177
DB 121 TVSSASTGSPVFLAPCSRSTSESTALGCLVKDYFPEPVVSWNSGALTSGVHTFPAV 180
QY 178 LOSGLYSLSSVVTVPSSSLGTQYTCNVDPKPSNTKYDKRVESKYGPCCSPAPEFLG 237
DB 181 LOSGLYSLSSVVTVPSSSLGTQYTCNVDPKPSNTKYDKRVESKYGPCCSPAPEFLG 239
QY 238 GPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVOFNNWYDGMVHNAAKTRPEQF 297
DB 240 GPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVOFNNWYDGMVHNAAKTRPEQF 299
QY 298 NSTYRVSVLTIVHQDLNGEKYKCKVSNKGLPAPIEKTISKAKGQPREPQVYTLPPSRE 357
DB 300 NSTFRVSVLTIVHQDLNGEKYKCKVSNKGLPAPIEKTISKAKGQPREPQVYTLPPSRE 359
QY 358 EMTKNQVSLTCLVKGFPYSDIAVEESNGQPENNYKTTIPVLDSDGSFFLYSRLTVDSKR 417
DB 360 EMTKNQVSLTCLVKGFPYSDIAVEESNGQPENNYKTTIPVLDSDGSFFLYSRLTVDSKR 419
QY 418 WQGNVFSQSVHMEALHNHYTQKSLSLSPGK 448
DB 420 WQGNVFSQSVHMEALHNHYTQKSLSLSPGK 450

RESULT 13
US-07-934-373C-23
Sequence 23, Application US/07934373C
Patent No. 5821337
GENERAL INFORMATION:
APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
```

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/ SOFTWARE: WinPacIn (Genentech)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/07/934,373C
/ FILING DATE: 21-Aug-1992
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US92/05126
/ FILING DATE: 15-JUN-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/715272
/ FILING DATE: 14-JUN-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Lee, Wendy M.
/ REGISTRATION NUMBER: 40,378
/ REFERENCE/DOCKET NUMBER: P0709P2
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 650/225-1994
/ TELEFAX: 650/952-9881
/ INFORMATION FOR SEQ ID NO: 23:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 469 amino acids
/ TYPE: Amino Acid
/ TOPOLOGY: Linear
/
US-07-934-373C-23

Query Match      84.6%; Score 2022; DB 2; Length 469;
Best Local Similarity 84.0%; Pred. No. 1.3e-154;
Matches 379; Conservative 31; Mismatches 37; Indels 4; Gaps 2;

QY 1 QVQLVQSGAEVKKRQSSVKVCASGYSFTSYVMHWRAQPGQGLEWIGYIYPNDGTY 60
DB 20 EVQLVESGGGLVQPGSRLSRATSGYTFETWMHMQAPGKLEWVAGINPKNGTSH 79
QY 61 NEKFKGRTITSDSTNTAYMELSLRSEDTAVYYCAR--EEYGNVYRFYDVGQGTLY 117
DB 80 NORFMDRFTISVDKSTSTAYMQMNSLRADFAVYYCARMKGALNGFDVRFYDVGQGTLY 139
QY 118 TVSSASTGSPVFLAPCSRSTSESTALGCLVKDYFPEPVVSWNSGALTSGVHTFPAV 177
DB 140 TVSSASTGSPVFLAPCSRSTSESTALGCLVKDYFPEPVVSWNSGALTSGVHTFPAV 199
QY 178 LOSGLYSLSSVVTVPSSSLGTQYTCNVDPKPSNTKYDKRVESKYGPCCSPAPEFLG 237
DB 200 LOSGLYSLSSVVTVPSSSLGTQYTCNVDPKPSNTKYDKRVESKYGPCCSPAPEFLG 258
QY 238 GPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVOFNNWYDGMVHNAAKTRPEQF 297
DB 259 GPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVOFNNWYDGMVHNAAKTRPEQF 318
QY 298 NSTYRVSVLTIVHQDLNGEKYKCKVSNKGLPAPIEKTISKAKGQPREPQVYTLPPSRE 357
DB 319 NSTFRVSVLTIVHQDLNGEKYKCKVSNKGLPAPIEKTISKAKGQPREPQVYTLPPSRE 378
QY 358 EMTKNQVSLTCLVKGFPYSDIAVEESNGQPENNYKTTIPVLDSDGSFFLYSRLTVDSKR 417
DB 379 EMTKNQVSLTCLVKGFPYSDIAVEESNGQPENNYKTTIPVLDSDGSFFLYSRLTVDSKR 438
QY 418 WQGNVFSQSVHMEALHNHYTQKSLSLSPGK 448
DB 439 WQGNVFSQSVHMEALHNHYTQKSLSLSPGK 469

RESULT 14
US-08-437-642B-23
Sequence 23, Application US/08437642B
Patent No. 6054297
GENERAL INFORMATION:
APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
```


Oy 358 EMTKNQVSLTCLVKGFPPSDIAVEMESNGOENNKTTPVLDSDSGSFELYSRLTVDKSR 417
Db 379 EMTKNQVSLTCLVKGFPPSDIAVEMESNGOENNKTTPMLDSDSGSFELYSRLTVDKSR 438
Oy 418 WQGNVFCSCSVWHEALHNHYTOKSLSLGK 448
Db 439 WQGNVFCSCSVWHEALHNHYTOKSLSLSPGK 469

Search completed: December 31, 2003, 10:33:11
Job time : 17.8548 secs